## STIC-Biotech/ChemLib

172599

<u>Μ</u>ε, '

From:

Li, Bao-Qun

Sent:

Monday, November 28, 2005 11:55 AM

To:

STIC-Biotech/ChemLib

Subject:

10,761,006

Please do the amino acid sequence homology and interference search against the nucleic acid sequence of SEQ ID NO:

1.

Bao Qun Li M.D

TC 1600°

Art Unit 1648

Tel. 517-272-0904

**REM, 3C18** 

Rm. 3D24

TOU/CHEM. DIV

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search

NA#\_\_\_\_\_ AA#:\_\_\_\_

S/L:\_\_\_\_ Oligomer:\_\_\_
Encode/Transl:\_\_\_

Structure #:\_\_\_\_ Text:\_\_
Inventor:\_\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\*\*\*\*\*
Vendors and cost where applicable
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DIALOG:\_\_\_
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WWW/Internet:\_\_\_
Other (Specify):\_\_\_\_\_

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MEDLINE=94120723; PubMed=8291231;
Norder H., Courouce A.M., Magnius L.O.;
Norder H., Courouce A.M., Magnius L.O.;
"Complete genomes, phylogenetic relatedness, and structural proteins of six strains of the hepatitis B virus, four of which represent two
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STRAIN-Genotype c;

Norder H.M.L.;

Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

L. Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

-! SIMILARITY: Contains 1 reverse transcriptase domain.

R EMBL; X75656; CAA53338.1; -; Genomic_DNA.

R GO; GO:0003877; F:DNA binding; IEA.

R GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-dependent DNA replication; IEA.

R GO; GO:0006278; P:RNA-dependent DNA replication; IEA.

R InterPro; IPR001462; DNApol_viral_C.

R InterPro; IPR001462; DNApol_viral_N.

R InterPro; PR00336; DNA_DOl_viral_N.

R Pfam; PF00336; DNA_DOl_viral_N; 1.
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Orthohepadnavirus.
NCBI_TaxID=10407;
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01-NOV-1996 (TrEMBLE). 01,
01-MAR-2004 (TrEMBLE). 26,
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-Q=/Cgn2_1/USPTO spool_p/US10761006/runat_01122005_113952_26669/app_query.fasta_1.3399
-Q=-Cgn2_1/USPTO spool_p/US10761006/runat_0112005_11-LGOPECL=0 -LGOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=bloeumeG -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-USRET=pc -NORM=ext -HRAPSIX=550 -MINLEN=0 -MAXLEN=2000000000
-USRET=pc -NORM=ext -HRAPSIX=550 -MINLEN=0 -MAXLEN=2000000000
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBICOK=100 -LONGLOG
-DEW TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -KGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FG\(^{*}\)EXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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2: uniprot_trembl:*
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seq length: 200000000
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                  core antigen.
Pfam; PF00078; RVT 1; 1.
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ç P	840	TAATAAAACCAAACGTTGGGGCTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTG 899
λō	8	TATTGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC 95
<b>Q</b> (	8 8	wproglnGluHislleValLeuLyslleLysGlnCysPheArgLysLeuPr 320
ž q	320	TGTAAATAGACCTATTGATTGATTGCTAAGAATTGTGGGTCTTTTGGGCTTTGC 1019
දු පු	1020	TGCCCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATC 1079
à	8	AGGCTITCACTITCTCGCCAACTTACAAGGCCTITCTGTGTAAACAATATCTGAA 11
qq	360	:
ර සි	1140	CCTTTACCCGGTTGCCCGGCAACGGTCCCGGTCTCTGCCAAGTGTTTGCTGACGCAACCCC 1199 
Š	00	GCCATAGGCCATCAGCGCATGGCTGGAACCTTTCTGGCTCTTTT 12
Dβ	400	
ò	1260	GCCGATCCATACTGCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGCGGGTCTGGAAA 1319
Db	420	ProlleHisThrAlaGluLeuLeuAlaAlaCysPheAlaArgSerArgSerGlyA
λ	1320	ACTIATOGGAACOGACACTOTGTIGTCCTCTCGGAAATACACCTCCTTTCCATGGCT 1379
qq	440	LeulleGlyThrAspAsnSerValValLeuSerArgLysTyrThrSerPheProTrp
λŏ	1380	GCTAGGGTGTGCTGCCAACTGGATCCTGCGCGGGACGTCCTTTGTCTACGTCCGGC 1439
qq	460	AsnTrp1leLeuArgGlyThrSerPheValTyrValProSerA
ζ	1440	GCTGAATCCCGCGGACCCGTCTCGGGGCCGTTTGGGGCTCTACCGTCCCCTTCTTCA 1499
qa	480	erArgGiyArgLeuGlyIleTyrArgProLeuLeu
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qq	200	ArgProThrThrGlyArgThrSerLeuTyrAlaValSerProSerValP
ζ	1560	TICTCATCTGCCGGACCGTGCGCTTCGCTTCACCTCTGCACGTCGCATGGAGACCACC 1619
qo	520	rHisLeuProAspArgValHisPheAlaSerProLeuHisValAlaTrpArgProP
οy	1620	CGCACGCCAGGTCTTGCCCAAGGTCTTATATAAGAGGAC
qq	540	
ò	1680	ATGTCAACGACCGACCTTGAGGCATACTTCAAAGACTGTGTGTTTAAAGACTGGGAGGAG 1739
qq	540	
λ	1740	TACTAGGAGGCTGTAGGCATAAATTGG
qq	540	540
č	1800	TGTTCACCAGCACCATGCAACTTTTTCTCCTCTGCCTAATCATCTCTCATGTTCATGTCCTA 1859
Db	540	
δ	1860	CTGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGACATGGACATTGACCCGTATA 1919
Db	540	540

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3060 CGGCGGTTTTTGGCGGGGGGGCCCTCAGGCTCAGGCATATTGACAACAGTGCCAGCAGCAGC
                                                  3120 ACCICCICCICCICCACCAATCGGCAGICAGGAAGACAGCCIACICCCAICTCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                   radecinace analysis of hepatitis B virus DNA in immunologically regative infection.";

Arch. Virol. 133:385-396 (1993).

L. SIMILARITY: Contains I reverse transcriptase domain.

-1- SIMILARITY: Cantains I reverse transcriptase domain.

C. 1- SIMILARITY: Cantains I reverse transcriptase domain.

RO; GO:0003677; F:DNA binding; IEA.

GO; GO:0004523; F:IDNA-directed DNA polymerase activity; IEA.

GO; GO:0004523; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0005723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0005729; F:RNA-dependent DNA replication; IEA.

RITHERPO; IPRO00201; DNAPOL_viral_C.

RITHERPO; IPRO00201; DNAPOL_viral_N.

RITHERPO; IPRO0047; RYTSe.

REPAM: PPRO034; DNA_DOL_viral_C; I.

REPAM: PPRO034; DNA_DOL_viral_N; I.

REPAM: PPRO034; DNA_DOL_viral_N; I.

REPAM: PRO00242; DNA_DOL_viral_N; I.
                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sub-type ayw;
MEDLINE=94079539; PubMed=8257295;
Preisler-Adams S., Schlayer M.J., Peters T., Hettler F., Gerok W.,
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726
49
57
243
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Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                          QG7907 HPBVO PRELIMINARY; PRT; 832 AA.
Q67907;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                  TCTAAGAGACAGTCATCCTCAGGCCACGCAGTGGAA 3215
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Conservative:
Mismatches:
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PROSITE; PS50878; RT_POL; 1.
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3745.50
72.16%
67.60%
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Hepatitis B virus.
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Best Local Similarity:
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TrpLeuGlnPheArgAsnSerGluProCysSerAspTyrCysLeuThrHisLeuValAsn 41
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                                                NUCLEOTIDE SEQUENCE.
STRAIN=Genotype e;
MEDLINE=94120723; PubMed=8291231;
MEDLINE=94120723; PubMed=8291231;
Morder H., Courouce A.M., Magnius L.O.;
"Complete genomes, phylogenetic relatedness, and structural proteins of six strains of the hepatitis B virus, four of which represent two
                                                                                                                                                                           STRAIN-Genotype 6.

A Norder H.M.L.

Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: Contains 1 reverse transcriptase domain.

EMBL; X75657; CAA53339.1; -; Genomic_DNA.

EMBL; X75657; CAA53339.1; -; Genomic_DNA.

GO; GO:0003877; F:DNA binding; IEA.

GO; GO:0003877; F:DNA binding; IEA.

GO; GO:0003878; F:NAN binding; IEA.

GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0006278; F:RNA binding; IEA.

GO; GO:0006278; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0006278; P:RNA-directed DNA polymerase activity; IEA.

InterPro; IPR001462; DNApol_viral_C.

InterPro; IPR001462; DNApol_viral_N.

InterPro; IPR00147; RVTSel.

R Pfam; PF00336; DNA_pol_viral_C; 1.

Pfam; PF00318; DNA_pol_viral_N; 1.

PRODOM; PD00078; RVT_1; 1.

PRODOM; PD00078; RVT_1; 1.

PROSOTE; PS00078; RYT_1; 1.

PROSOTE; PS0078; RYT_1; 1.
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  Retro-transcribing viruses; Hepadnaviridae;
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Matches:
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Virology 198:489-503(1994).
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  Viruses; Retro-tra
Orthohepadnavirus.
NCBI_TaxID=10407;
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111 TTPLeuSerleuAspvalSerAlahlabheTytHisleubroLeuHisProhlahlabke 42 GCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	8 8 8 8 8 8	8 8 8	6 8 6 8 6	6 6 6	8 & 8 &	8 6 8 6	8 4 8 4 8 4 8 4 8
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Pred. No.:
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GlyGluGluTyrPheHisHisGlnSerSerGlyIlePheSerArgProProValGlySer
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Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen D.-S.;
Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen D.-S.;
Submitted (CTT-2002) to the EVBL/GenBank/DDBJ databases.

EMBL; AY167095; AAO41311.1; -; Genomic_DNA.

RG O; GO:0003677; F:DNA-binding; IEA.

RG) GO:0003671; F:DNA-directed DNA polymerase activity; IEA.

RG) GO:0004519; F:ENDA-directed DNA polymerase activity; IEA.

RG) GO:0004519; F:Hydrolase activity; IEA.

RG) GO:0004529; F:Hydrolase activity; IEA.

RG) GO:000373; F:Hydrolase activity; IEA.

RG) GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

RG) GO:000578; F:RNA-dependent DNA replication; IEA.

RG) GO:0006279; P:RNA-dependent DNA replication; IEA.

RICEPPO; IPR000401; DNApol_viral_C.

InterPro; IPR000477; RVTSe.
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OTIORS;
01-0CT-2003 (TEMBLrel. 25, Created)
01-0CT-2003 (TEMBLrel. 25, Last sequence update)
01-0T-2003 (TEMBLrel. 26, Last annotation update)
Polymerase protein.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBL_TAXID=10407;
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Matches:
Conservative:
Mismatches:
Indels:
Pfam; PF00336; DNA_pol_viral_C; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00078; RVT_1; Z.
ProDom; PF000181; DNApol_viral_C; 1.
SEQUENCE 843 AA; 9447] MW; A40B9C18D84B4EA5
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Best Local Similarity:
Query Match:
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J. Infect. Dis. 191:2022-2032(2005).
EMBL; DQ089793; AAZ05280.1; -; Genomic DNA.
SEQUENCE 843 AA, 94494 MW; BB50233DFEBA4E29 CR
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Conservative:
Mismatches:
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Tsuda F., Miyakawa Y., Mayumi M.;

"Nuclectide Sequence of a Cloned Hepatitis B Virus Genome ,Subt;
"Nuclectide Sequence of a Cloned Hepatitis B Virus Genome ,Subt;
"T ayr:Comparison with Genomes of the Other Three Subtypes.";
"J. Gen. Wizison with Genomes of the Other Three Subtypes.";
"C -!- SIMILARITY: Contains 1 reverse transcriptase domain.

R MBH; X04615; CAA2286.1; -; Genomic_DNA.

R MGO: GO:0003577; F:DNA binding; IEA.

R GO; GO:0003777; F:DNA-directed DNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003564; F:RNA-dependent DNA replication; IEA.

R InterPro; IPR001462; DNApol_viral_C.

R InterPro; IPR00147; RVISe.

R Pfam; PF00075; RVIT_1; I.
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STRAIN=AYY;
MEDLINE=87059755; PubMed=3783127;
Okamoto H., Imai M., Shimozaki M., Hoshi Y., Iizuka H., Gotanda
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059026 HPBVO PRELIMINARY; PRT; 540 AA.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
P gene product (Fragment).
Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
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Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Matches:
Conservative:
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NUCLEOTIDE SEQUENCE
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                                 GGGTACTTTACCGCAGGAACATATTGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC
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                                                                                                                                  aleuAsnProAlaAspAspProSerArgGlyArgLeuGlyLeuTyrArgProLeuLeuHi
                                                           TTCTCATCTGCCGGACCGTGTGCACTTCGCTTCACCTCTGCACGTCGCATGGAGACCACC
                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
P protein [Includes: DNA-directed DNA polymerase (EC 2.7.7.7); RNA-directed DNA polymerase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIBE SEQUENCE [GENOMIC DNA].

NUCLECTIBE SEQUENCE [GENOMIC DNA].

MEDLINE=83168919; PubMed=6300776;

Ono Y., Onda H., Saeada R., Igarashi K., Sugino Y., Nishioka K.;

"The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype adr and adw.";

Nucleic Acids Res. 11:1747-1757(1983).

-!- CATALYTIC ACTIVITY: Deoxynucleoside triphosphate + DNA(n) = diphosphate + DNA(n+1).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
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PROSITE; PS50878; RT_POL; 1.

DNA replication; DNA-binding; DNA-directed DNA polymerase;

Endonuclease; Hydrolase; Multifunctional enzyme; Nuclease;

Nucleotidyltransferase; RNA-directed DNA polymerase;

DOMAIN 357 600 Reverse transcriptase.

SEQUENCE 843 AA; 94400 MW; A6B2D490839C4EBB CRC64;
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Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
NCBI_TaxID=106820;
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Matches:
Conservative:
Mismatches:
Indels:
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PIR; A00704; JDVLVR.
InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVTse.
Pfam; PF00215; DNA_pol_viral_C, 1.
Pfam; PF00215; DNA_pol_viral_N, 1.
Pfam; PF00215; DNA_pol_viral_N; 1.
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MEDLINE=95294549; PubMed=7775946;
Uchida T., Gotoh K., Shikata T.;
Uchida T., Shikata T.;
Uchida T GATCCATACTGCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAACT 097975, HPBVO PRELIMINARY; PRT; 540 AA.
097975, O1-PBB-1997 (TrEMBLrel. 02, Created)
01-PBB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0RF (Fragment).
Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI\_TAXID=10407; 540 AA; 60346 MW; 7BBE285359DD39C5 CRC64;

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TGTAAATAGACCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGGTCTTTTGGGCTTTGC 1019
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R GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0004519; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0004519; F:endonuclease activity; IEA.

GO; GO:0004523; F:monuclease activity; IEA.

GO; GO:0003523; F:monuclease H activity; IEA.

GO; GO:0003954; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0000519; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0000519; F:RNA-dependent DNA replication; IEA.

InterPro; IPR00140; DNApol_viral_N.

InterPro; IPR00047; RVISe.

R Pfam; PF00242; DNA_pol_viral_C; 1.

Pfam; PF00242; DNA_pol_viral_N; 1.

Pfam; PF000184; NVT_1; 1.

R Pfam; PF000184; NVT_1; 1.

R Pfam; PF000184; NVT_1; 1.

R Pfam; PF000184; NVT_1; 1.
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Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen D.-S.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, AN167096; AA041314.1; -; Genomic_DNA.

GO; GO:0003687; F:DNA-binding; IEA.

GO; GO:0004519; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0004519; F:ndonuclease activity; IEA.

GO; GO:0004519; F:ndonuclease activity; IEA.

GO; GO:0004519; F:NNA-directed DNA polymerase activity; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000578; F:RNA-dependent DNA replication; IEA.

GO; GO:000578; F:RNA-dependent DNA replication; IEA.

R InterPro; IPR000401; BNApol_viral_C.

R InterPro; IPR000401; RVTse.

R Pfam; PP00078; RVT=1; Z.

R Pfam; PP00078; RVT=1; Z.

R Probom; PD0000814; DNApol_viral_C; 1.

R Probom; PD0000814; DNApol_viral_C; 1.

R Probom; PD0000814; DNApol_viral_C; 1.
01-MAR-2004 (ILEMINA)
Polymerase protein.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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RY Dubmed=15368435; DOI=10.1002/hep.20331;

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BY GO; GO:0003877; Provided 1: -; Genomic_DNA.

BY GO; GO:0004519; Provided BN polymerase activity; IEA.

BY GO; GO:0004519; Provided BN polymerase activity; IEA.

BY GO; GO:0005732; PriNA binding; IEA.

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BY GO; GO:0006740; PriNA binding; IEA.

BY GO; GO:000578; PRINA-directed DNA polymerase activity; IEA.

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RA Uchida T., Aye T.T., Shimojima M., Gotoh K., Shikata T.;
RA Uchida T., Aye T.T., Shimojima M., Gotoh K., Shikata T.;
RA Uchida T., Aye T.T., Shimojima M., Gotoh K., Shikata T.;
RT "Full-length nucleotide sequence of a hepatitis B virus (HBV) mutant
RT isolated from a patient with acute hepatitis who did not exhibit
RT serological markers for HBV infection.";
RL Int. Hepatol. Commun. 2:70-73(1994).

BR GO; GO:0003677; F:DNA binding: IEA.

BR GO; GO:0004519; F:DNA-directed DNA polymerase activity; IEA.

BR GO; GO:0004519; F:RNA-directed DNA polymerase activity; IEA.

BR GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

BR GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

BR GO; GO:0006778; P:RNA-directed DNA polymerase activity; IEA.

BR GO; GO:0006778; P:RNA-directed DNA replication; IEA.

BR GO; GO:0006778; P:RNA-directed DNA replication; IEA.

BR GO; GO:000739; P:RNA-directed DNA replication; IEA.

BR FEAM: PF00036; DNA_DOI_viral_C; 1.

BR FEAM: PF00078; RVT 1; 2.

BR PRODON: P0000844; DNA_DOI_viral_C; 1.

BR PRODON: P0000844; DNA_DOI_viral_C; 1.

BR PRODON: P0000844; DNA_DOI_viral_C; 1.

BR PRODON: P0000844; DNA_DOI_viral_C; 1.
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MEDLINE=93096607; PubMed=1461746;
Mukaide M.;
"The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and phylogenetic analysis.";
Nucleic Acids Res. 20:6105-6105(1992).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NNV-1996 (TrEMBLrel. 26, Last annotation update)
DNA polymerase.
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TAXID=10407;
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Length: Matches: Conservative: Mismatches: Indels:

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Pfam; PF00078; RVT 1; 2.
ProDom; PD000814; DNApol viral C; 1.
SEQUENCE 843 AA; 94462 MW; IBCCF79639BB140D CRC64;
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MEDLINE=97160188; PubMed=9007704; DOI=10.1016/S0168-8278(96)80280-7; Asahina Y., Enomoto N., Kurosaki M., Sakuma I., Izumi N., Marumo F., Sato C.;

Sato C.;

"Sequential changes in full-length genomes of hepatitis B virus accompanying acute exacerbation of chronic hepatitis B.";

"Sequential changes in full-length genomes of hepatitis B virus accompanying acute exacerbation of chronic hepatitis B.";

"Hepatol. 25:787-794(1996).

"The patol. 25:787-794(1996).

"EMBL; D50518; BAA23435.1; -; Genomic_DNA.

"BMBL; D50517; BAA23435.1; -; Genomic_DNA.

"GO; GO:000367; F:DNA-directed DNA polymerase activity; IEA.

"GO; GO:0004519; F:HNA-directed DNA polymerase activity; IEA.

"GO; GO:0004519; F:RNA-directed DNA polymerase activity; IEA.

"GO; GO:0004523; F:RNA-dependent DNA replication; IEA.

"GO; GO:000578; P:RNA-dependent DNA replication; IEA.

"InterPro; IPR000471; RVT8a.

"InterPro; IPR000477; RVT8a.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 29, Last annotation update)
101-FBB-2005 (TrEMBLrel. 29, Last annotation update)
101-JAN-1998 (TrEMBLrel. 29, Last annotation update)
101-JAN-1998 (TrEMBLrel. 29, Last annotation update)
101-TBB-2005 (TrEMBLrel. 20, Last annotation update)
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DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype adr)
C;Species hepatitis B virus, HBV
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A00704
B;Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Sugino, Y.; Nishioka, K.
Nucleic Acids Res. 11, 1747-1757, 1983
A;Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype A;Reference number: A93460; MUID:83168919; PMID:6300776
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A;Residues: 1-843 < CNO>
C;Superferences: UNIPROT:P03157; UNIPARC:UPI00001297FE
C;Superfemily: hepatitis virus DNA-directed DNA polymerase
C;Reywords: DNA biosynthesis; nucleotidyltransferase
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-G=/CGDT 1/10SPTO spool p/US10761066/runat_01122005_113953_26882/app_query.fasta_1.3399
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184 ACCCTGCTGGTGTTACAGGGGGTTTTTCGTTGACAAAATCCTCACAATACCGCA 243 	GAGTCTAGACTCTG-GRGGACTTCTCTCAGAGGGGAGCACCCACGTGTTCCTG	GCCAAATTGGCAGTCCCCAACTCCCATCACCACCACCTTTGTCTTTGTCTTTGTTTTGTCTTTTTTTT	CTGGCTATCGCTGGTGTCTGCGGCGTTTTATCATATCCTCTTCATCCTGCTGCTAT	423 GCCTCATCTTCTTGTTGGTTCTTCTGGACTACCAGGTATGTTGCCCGTTTGTCCTCTAC 482 	483 TTCCAGGAACATCAACCACGGGGCCATGCAAGACCTGCACGACTCCTGCTCAAG 542 	543 GAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAACGCGAAACTGCACTTGTA 602 	603 TICCCATCCCATCATCTGGGGTTITCGCAAGATTCCTAIGGGAGTGGGCCTCAGTCCGTT 662 	663 TCTCCTGGCTCTGTTTACTAGTGCCATTTGTTCAGTGGTTGGT	723 TTTGGCTTTCAGTTATATGGATGATGATGGGGGCGGAGGTCTGTACAACATCTTGA 782 	783 GTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATACATTTAAACCCTAA 842 	843 TAAAACCAAAGGTTGGGGCTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTGGGG 902 	903 TACTITACCGCAGGAACATAITGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCCTGT 962 	963 AAATAGACCTATTGATTGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTGCTGC 1022 	1023 CCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATCTAA 1082 	1083 GCAGGCTTTCACCTCCCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAACCT 1142 	1143 TTACCCCGTTGCCCGGCAACGGTCCGGTCTCTGCCAAGTGTTTGCTGACGCAACCCCCAC 1202 	1203 IGGATGGGGCTTGGCCATAGGCCATCAGCGCATGGCTCGAACCTTTCTGGCTCCTCTGCC 1262 
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RESULT S35527 DNA-di. C;Spec	RESULT 2 S35527 DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype adr) C;Species: hepatitis B virus, HBV
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C; Ac	cession: S35527 kaidė, M.; Kumazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.
Nuci A;Ti A;Re	eic Acids Kes. 20, 6105, 1992. Lle: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and E. ference number: S35527; MUID:93096607; PMID:1461746
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A; We A; Re A; Cr	lecule type: DNA Salduses: 1-843 «MUK» oss-references: UNIPROT:Q81107; UNIPARC:UPI00000EED31; EMBL:D12980; NID:9221500; PIDN
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C, Ge C, Su C, Su C, Ke	netics: trons: 345/3 perfamily: hepatitis virus DNA-directed DNA polymerase ywords: DNA biosynthesis; nucleotidyltransferase
Allig Pred Scor Perc Best	Alignment Scores:  Pred. No.: 2.44e-198 Length: 843 Score: 2789.00 Matches: 523 Percent Similarity: 98.15% Conservative: 8 Best Local Similarity: 96.67% Mismatches: 9 Onery Match: 47.22% Indels: 2
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.;Crosidues: 1-843 -LONA
.;Crosis-references: UNIPROT:QG7952; UNIPARC:UPI00000EB7B3; EMBL:X52939; NID:g457780; PI:
.;Experimental source: subtype adr
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C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
A;Variety: subtype adr
C;Actes O'S-Sep-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C;Accession: 843491
R;Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acids Res. 18, 4940, 1990
Nucleic Acids Res. 18, 4940, 1990
N;Title: Sequence of a replication competent hepatitis B virus genome with a preX open 1, Reference number: S12598; MUID:90370503; PMID:2395664
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';Gene. P; pol
';Superfamily: hepatitis virus DNA-directed DNA polymerase
';Keywords: DNA biosynthesis; nucleotidyltransferase
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384 ThrG	300 CTGG      403 rTrp	360 GTCC      423 uSer	420 TATG      443 aMet	480 TACT      463 rThr	540 AAGG  ::: 483 rLys	600 GTAT      503 uTyr	660 GTTT      523 oPhe	720 CTGT      543 8CY8	780 TGAG      563 uGlu	840 TAAT      583 OABD	900 GGGT      603 pGly	960 TGTA      623 oval	1020 TGCC      643 aAla	1080 TAAG      663 rLys	1140 CCTT      683 nLeu	1200 CACT      703 oThr	1260 GCCG      723 uPro	1320 ACTT

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DNR-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype adr, mutant) Cispecies: hepatitis B virus, HBV Cispecies: hepatitis B virus, HBV Cispecies: hepatitis B virus, HBV Cispecies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 Ciscossion: 804568 Rikho, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S. Nucleic Acids Res 17, 2124, 1989 A.Fitle: The nucleotide sequence and reading frames of a mutant hepatitis B virus subtyp A; Accession: 804568; MUID:89183619; PMID:2928116 A; Accession: 804568 A; Ascetus: translation not shown A; Molecule type: DNA
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              UleuGlyCysAlaAlaAsnTrpIleLeuArgGlyThrSerPheValTyrValProSerAl
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A;Cross-references: UNIPROT:P31870; UNIPARC:UPI00001297FB;
C;Superfamily: hepatitis virus DNA-directed DNA polymerase
C;Keywords: DNA biosynthesis; nucleotidyltransferase
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	RESULT 5 T13473 T13473 T13474 DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (isolate 29Y11HCC) C; Species: hepatitis B virus, HBV A; Variety: isolate 29Y11HCC C; Date: 13-apg-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C; Accession: T13473 R; Takahashi, K; Akahane, Y; Hino, K; Ohta, Y; Mishiro, S.	Arritle: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin A; Title: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin A; Reference number: Z17684; MUID:99129050; PMID:9930189 A; Accession: T13473 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-825 cTAK> A; Cross-references: UNIPROT:Q9YZS3; UNIPARC:UPIO0000F4BF5; EMBL:AB014388; NID:g3582381;	A; Experimental Source: Japanese patient with nepatocellular carcinoma 1801ate 2911IHUU Cafforetics: A;Genetics: P. A;Gene: P. A;Introns: 303/3 C;Superfamily: hepatitis virus DNA-directed DNA polymerase C;Keywords: DNA biosynthesis; nucleotidyltransferase Aliqument Scores:	Pred. No.: 7.33e-191 Length: 825 Score: 2688.00 Matches: 504 Percent Similarity: 95.92% Mismatches: 13 Best Local Similarity: 93.51% Mismatches: 21 Query Match: 45.51% Indels: 2 DB: 2 US-10-761-006A-1 (1-3215) x T13473 (1-825)	Qy         7 AACATICCACCAAGCTCTGCTAGATCCCAGGGTGAGGGGCCTATATTTCCTGCTGGTGG 66           ::::::::::::::::::::::::::::::::::::	Qy         127 CTCGAGGACTGGGGACCCTGCACCGAACATGGAGATTCCTAGGATTCCTAGGACC 186	Db 348 Prohlafill[	Qy 306 AAAATTGGCAGTCCCCAACTCCCCAACCTCTTGTCCTCCAATTTGTCCTG 365
360 GTCCTGGCTATCGCTGGATGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGC 419	GTATTCCCATCCATCATCCTGGGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCC 65	720 CTGTTTGGCTTTCAGTTATGGATGATGGTATTGGGGGCGAAGTCTGTACAACATCT 779	840 TAATAAAACCAAACGTTGGGGCTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTG 899	TGTAAATAGACCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTGC TGTAAATAGACCTATTGGAAGTATGTCAAAGAATTGTGGGGTCTTTGGGGCTTTGC OVALASAAATGPTOLISASGTTDLYSVALCYSGINAYGILSVALGIYLEUGLYPheAl TGCCCCTTTTACACAATGGCTATCCTGCCTTGATGCCTTTATATGCATGTATAAATC	1080 TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAA 1139		722 uProlleHisThrAld[	1380 GCTAGGGTGCTGCCAACTGGATCCTGCGGGACGTCCTTTGTCTACGTCCGGC 1439
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Db 767 nProAlaAspA  Qy 1506 GTTCCGGCCGA	A, Variety: isolate 090094 C, Date: 13-Aug-1999 #sequ C, Accession: T13468 R, Takahashi, K.; Akahane, Arch. Virol. 143, 2313-23 A, Title: Hepatitis B viru A, Reference number: 21768 A, Accession: T13468 A, Status: preliminary; tr A, Molecule type: DNA A, Residues: 1-827 < TAK> A, Cross references: UNIPR		DB:  US-10-761-006A-1 (1-3215)  QY	Qy         130 GAGGACTGGGG           Db         331 GluAspTrpGl           Qy         190 GCTGGTGTTAC           Db         351 AlaArgValTh           Qy         250 AGACTCTG-GT           Db         371 ArgLeuValVa	Oy 309 ATTCGCAGTCC
	CCATCCCATCATCCTGGGGCTTTCGCAAGATTCCTATGGGGGTGGGCCTCAGTCCGTTTCT		966 TAGACCTATTGAAAGTANTGTCAAAGAATTGTGGGTCTTTTGGGCTTTGCTGCCCC 1025 607 nArgProlleAspTrpLysValCysGlnArg1leValGlyLeuLeuGlyPheAlaAlaAlaPr 627 1026 TTTTACACAATGTGGCTACCTTGATGCCTTTATACAACTAAAACAATCTAAAGCA 1085 627 OPHeThrGlnCysGlyTyrProAlaLeuMetProLeuTyrAlaCysIleGlnSerLysGl 647 1086 GGCTTTCACTTTCTGCCAACTTACAAGCCTTTCTGTGAAACAATATCTGAACCTTTA 1145 647 nAlaPheThrPheSerProThrTyrLysAlaPheLeuCysLysGlnTyrLeuAsnLeuTy 667	1146 CCCCGTTGCCCGGCAACGGTCCTCTGCCAAGTGTTTGCTGACGCAACCCCCACTGG 1205	1326 CGGAACCGACAACTCTGTTGTCCTCTCCGGAATACACCTCCTTTCCATGGCTGCTAGG 1385
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cus genomic sequence in the circulation of hepatocellular carcinc 884; MUID:99129050; PMID:9930189
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                          ACCACGGGGGCACCTCTTTACGCGGTCTCCCCGTATGTGCCTTCTCA 1565
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1326, 1998
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DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype ayw, isolate patic; Species: hepatitis B virus, HBV
C; Species: hepatitis B virus, HBV
A; Variety: subtype ayw, isolate patient C1005
C; Date: 0.6 Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C; Accession: 871785
R; Preisler-Adams, S.; Schlayer, M.J.; Peters, T.; Hettler, F.; Gerok, W.; Rasenack, J. submitted to the EMBL Data Library, March 1993
A; Description: Identification and sequence analysis of hepatitis B virus DNA in immunol A; Reference number: 832202
A; Reference number: 832202
A; Residues: 1-832 <PRES
A; Accession: 871785
A; Residues: 1-832 <PRES
A; Residues: 1-832 <PRES
A; Coss-references: UNIPROT: QB/N11; UNIPROT: Q9IF40; UNIPROT: Q96846; UNIPROT: Q67892; UNIPROT: Q58040; UNIPROT: Q5684; UNIPROT: Q5 A; Experimental source: subtype ayw, isolate patient C1005
C; Superfamily: hepatitis virus DNA-directed DNA polymerase
C; Reywords: DNA biosynthesis; nucleotidyltransferase
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y da	600 GTATTCCCATCATCCTGGGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCC 659	KESULT 8 JDVLVB DNA-directed DNA C;Species: hepat
<u>ک</u> و	660 GTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCA 119 	A,Note: host Home C,Date: 17-Mar-19 C,Accession: A00' R,Bichko, V.; Pu
දු දු	720 CTGTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGGCGAAGTCTGTACAACATCT 779 	FEBS Lett. 185, A;Title: Subtype A;Reference numb A;Accession: A00
λ O O	780 TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGCTTTTGGGTATACATTTAAACCC 839	A; Molecule type: A; Residues: 1-83; A; Cross-reference C; Superfamily: ho
λ <mark>ο</mark> qα	840 TAATAAAACCAAACGTIGGGGCTACTCCTTAACTTCATGGGATATGTAATTGGAAGTTG 899 572 OASnLysThrLysArgTrpGlyfyrSerLeuHisPheMetGlyfyrValIleGlySerTy 592	C; Keywords: DNA ] Alignment Scores Pred. No.:
& 4a	900 GGGTACTTTACCGCAGGAACATATGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC 959 	Score: Percent Similarit Best Local Simila Query Match:
S a	960 IGTAAATAGACCTATTGATTGGAAAĞTATGTCAAAGAATTGTGGGTCTTTTGGGCTTTTGC 1019  :::	US-10-761-006A-1
85 Q	1020 TGCCCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATC 1079	293
\$ 6 6	1080 TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGAAACAATATCTGAA 1139 	
දු පු	1140 CCTTTACCCCGTGCCGGCAACGGTCTCTGCCAAGTGTTTGCTGACGCAACCCC 1199 	Oy 121 AA: 
දුරු දුර	1200 CACTGGATGGGGCTTGGCCATGGCGATGGCTGGAACCTTTCTGGCTCCTCT 1259	Oy 181 AG 
ර් සි	1260 GCCGATCCATACTGCGGAACTCCTAGCTGTTTTGCTCGCAGCCGGTCTGGAGCAAA 1319 	Qy 241 GCJ 
දු දු	1320 ACTTATCGGAACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTCCATGGCT 1379 ::::::	992 rT.
Q Qq	1380 GCTAGGGTGTGCCAACTGGATCCTGCGGGGGCGTCCTTTGTCTACGTCCGTC	Oy 360 GTV 
ço da	1440 GCTGAATCCCGGGGACCCGTCTCGGGGCCGTTTGGGGCTCTACCGTCCCCTTCTTCA 1499	Qy 420 TA:     Db 432 aMe
ço O	1500 TCTGCCGTTCCGGCCGACGGGCGCACCTCTCTTACGCGGTCTCCCCGTATGTGC 1559	
λ Q Q	1560 TTCTCATCTGCCGGACCGTGTGCACTTCGCTTCTGCACGTCGCATGGAGACCACC 1619	Oy 540 AA(          Db 472 rAi
දු පු	1620 G 1620 832 o 832	Oy 600 GTI 

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32 <BIC>
ces: UNIPROT:P03156; UNIPARC:UP100001710E8; GB:X02496; NID:g62280; PIDN:C
hepatitis virus DNA-directed DNA polymerase
biosynthesis; nucleotidyltransferase
 B virus (subtype ayw, strain pHB320
                                                                                      structure analysis.
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A polymerase (EC 2.7.7.7) - hepatitis B virus (subtype ayw, stitis B virus, HBV men sapiens (man)
men sapiens (man)
1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                               GGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTCGTTGACAAGAATCCTCACAATACC
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                                                                     208-212, 1985
e ayw variant of hepatitis B virus: DNA primary
bber: A05237, MUID:85204397, PMID:3996597
0703
:: DNA
                                                           ishko, P.; Dreilina, D.; Pumpen, P.; Gren, E.
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QY         660 GTT           QY         512 OPH           QY         720 CTG           QY         720 CTG           QY         720 CTG           QY         780 TGA           QY         840 TAA           QY         840 TAA           QY         960 GGG           QY         1020 TGC           QY         1020 TGC           QY         1120 GCC           QY         1120 GCC           QY         1132 ACT           QY         1132 ACT           QY         1132 ACT           QY         1130 GCT           QY         1140 GCT           QY         1150 GCT           QY         150 GCT           QY         150 GCT           QY         150 GCT           QY         150 GCT           QY         1620 G1           QY         1620 G1           QY         1620 G1           QY         1620 G1           QY         1620	C.Date: 2   C.Date: 2   C.Date: 3   C.Da	SUDMITTEGETTTCAGTTATATGGATATGATGATGTATTGGGGGGGAAGTCTGTACAACATCT 779 A; Description of the control of the cont	839	89	959	1019	TGCCCCTTTTACACAATGTGGGTATCCTGCCTTGATGCCTTATATGCATGTATACAATC 1079   US-10-76:   US-10-76:	1139 672	1199	nLeuTyrFroValAlaargGinArgFroGlyLeuCy8GinValPheAlaA8PAlaThrFr	euAlaArgie 712	GCCGATCCATACTGCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAA 1319	ACTTATCGGAACCGACAACTCTGTTGTCTCTCTCGGAAATACACCTCCTTTCCATGGCT 1379 ::::::	1439	772			uProPheArgProthrThrdlyArgThrSerLeuTyrAlaAspSerProSerValPr 812	TTCTCATCTGCCGGACCGTGCACTTCGCTTCTCGCTCTCGCACGTCGCACGACCACC		32 0y	q <sub>0</sub>	polymerase (BC 2.7.7.7) - hepatitis B virus (subtype ayw4)
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23-Nov-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004 sion: S47406 enniczak, A. ento the EMBL Data Library, August 1994 ed to the EMBL Data Library, August 1994 iption: Molecular cloning and sequencing of two complete genomes of polish isola ence number: S47404 sion: S47406
                                                                        ule type: DNA
Mess 1-822 «FUL»
-references: UNIPROT:Q67892; UNIPARC:UPI00000EF97E; EMBL:Z35716; NID:g527435; PI
imental source: subtype ayw4
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                                                                                                                                 family: hepatitis virus DNA-directed DNA polymeraserds: DNA biosynthesis; nucleotidyltransferase
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Matches:
Conservative:
Mismatches:
Indels:
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Nature 281, 646-650, 1979 A;Title: Nucleotide sequence of the hepatitis B virus genome (subtype ayw) in E. A;Reference number: A93214; MUID:81012091; PMID:399327

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A/Recession: A00702

A/Recession: A00702

A/Recession: A00702

A/Residues: 1-832.44; MOID: 010.2071; FRID: 3532.7

A/Residues: 1-832.464L.

A/Esperimental source: cloned in Escherichia coli

R/Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.

A/Residues: 220745

A/Recession: S20748

A/Recession: S20748

A/Recession: S20748

A/Recession: S20748

A/Residues: 1-276,'S',278-292,'L',294-458,'H',460-465,'N',467-469,'S',471-612,'V',614-67

A/Residues: 1-16,'D',119-223,'C',225-245,'M',247-271,'Q',273-277,'D',279-291

A/Residues: 1-16,'D',118-117,'N',119-223,'C',225-245,'M',247-271,'Q',273-277,'D',279-291

A/Residues: 1-16,'D',118-117,'N',119-223,'C',225-245,'M',247-271,'Q',273-277,'D',279-291

A/Residues: DAA

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C;Superfamily: hepatitis virus DNA-directed DNA polymerase C;Keywords: DNA biosynthesis; nucleotidyltransferase

Gene: P

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483 TTCCAGGAACATCAACCACCAGGAGCCATGCAAGACCTGCACGACTCCTGCTCAAG 542
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DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype .C.species: hepatitis B virus, HBV

A;Variety: subtype abtype abtype subtype suptype c;Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text_change 09-Jul C;Accession: A00702; S20748; S53131

R;Gallbert, F.; Mandart, E.; Fitoussi, F.; Tiollais, P.; Charnay, P.
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302

393

183 353 243 373

333

313

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Length: Matches: Conservative: Mismatches: Indels:

1.58e-187 2643.00 95.00% 91.30% 44.74%

Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

Alignment Scores:

Pred. No.:

US-10-761-006A-1 (1-3215) x JDVLVA (1-832)

362 413 422

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GITTCTCCTGGCTCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCCA 719

Thu Dec 29 19:54:04 2005

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<u>ک</u> ۾	720	CTGTTTGGCTTTCAGTTATATGGGATGATGTGGGGGCGAAGTCTGTACAACATCT 779	
S G	780	TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATACATTTAAACCC 839	
& 8	840 583	TAATAAAACCAAACGTTGGGGCTACTCCCTTAACTTCATGGGATATGTAATTGGAAGTTG 899	
දු දු	900	GGGTACTTTACCGCAGGAACATATTGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC 959 	
à a	960	IGTAAATAGACCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGTCTTTTGGGCCTTTGC 1019 	
& a	1020	TGCCCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATC 1079	
S &	1080	TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAA 1139 	
S S	1140	CCTTTACCCCGTTGCCGGCAACGGTCCTGTGCCAAGTGTTTGCTGACGCAACCCC 1199	
P &	1200	CACTGGATGGGGCTTGGCCATGGCGCATGGCTGGAACCTTTCTGGCTCCTCT 1259	
S G	1260	GCCGATCCATACTGCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAA 1319 	
S S	1320	ACTTATCGGAACCGACAACTCTGTTGTCCTCTCGGAAATACACCTCCTTTCCATGGCT 1379	
ç q	1380		
S G	1440	GCTGAATCCCGGGACGACCCGTCTCGGGGCCGTTTGGGGCTCTACCGTCCCCTTCTTCA 1499	
& a	1500	TCTGCCGTTCCGGCCGACCACGGGCGCACCTCTCTTTACGCGGTCTCCCCGTATGTGCC 1559	
<u>ئ</u> ۾	1560	TTCTCATCTGCCGGACCGTGTGCACTTCGCTCTGCACGTCGCATGGAGCCACC 1619	
දු සි	1620	G 1620 G 1843	
RESULT 1 JDVLA1 DNA-dire C;Specie C;Date: C;Accese	12 ected res: her 30-Ser	NESULT 12 JUVLA1 DNN-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (strain alpha1) C;Species: hepatitis B virus, HBV C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004 C;Accession: C34773	

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R;Tong, S.; Li, J.; Vitvitski, L.; Trepo, C.
Vitology 176, 580-603, 1990
A;Title: Active hepatitis B virus replication in the presence of anti-HBe is associated A;Title: Active hepatitis B virus replication in the presence of anti-HBe is associated A;Reference number: A34773, MUID:90266476; PMID:2345966
A;Accession: C34773
A;Accession: C34773
A;Residues: Lranslation not shown
A;Molecule type: DNA
A;Residues: 1-832 <TON>
A;Cross-references: UNIPROT:P24024; UNIPARC:UPI00001297F7; EMBL:M32138; NID:g329667; PID
C;Genetics:
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                                                                                                                       A.Gene: P
C.Superfamily: hepatitis virus DNA-directed DNA polymerase
C.Keywords: DNA biosynthesis; nucleotidyltransferase
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Matches:
Conservative:
Mismatches:
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PID

UNIPARC:UPI00000F25B1; EMBL:X65259; NID:g59439; patient E

832 244 25 44 0

Length: Matches: Conservative: Mismatches: Indels:

(1-832)

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A;Reference number: S20745
A;Accession: S20757
A;Molecule type: DNA
A;Residues: 1-832 (LAL)
A;Cresidues: 1-832 (LAL)
A;Experimental source: Subtype ayw, patient E
C;Genetics:
A;Gene: C
C;Genetics:
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DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype ayw, patient
CiSpecies: hepatitis B virus, HBV
A.Variety: subtype ayw, patient B
CiSpace: 20-Peb-1995 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
CiAccession: S20757
Filai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Melis, A.; Porru, A.
submitted to the EMBL Data Library, March 1992
A;Description: Sequence analysis of HBV genomes isolated from patients with HBsAg n
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RESULT 14 867505 DNA-directed DNA polymerase (EC 2.7.7.7) - hepatitis B virus (subtype ayw3, is cypecies: hepatitis B virus, HBV C;Species: hepatitis B virus, HBV A;Variaty: subtype ayw3, isolate Hope CH1357 C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004 C;Accession: 867508 R;Norder, H.; Ebert, J.W.; Fields, H.A.; Mushahwar, I.K.; Magnius, L.O. Virology 218, 214-223, 1996 A;Tele: Complete sequencing of a gibbon hepatitis B virus genome reveals a un A;Reference number: 867503; MUID:96207410; PMID:8615024 A;Accession: 867505 A;Molecule type: DNA	isolate Hope unique genot	8 8 8 8 8 8	600 GTATTCCCATCATCCTGGGGCTTTCGCAAGATTCCTATGGGGGCCTCAGTCC 659

C;Superfamily: hepatitis virus DNA-directed DNA polymerase C;Keywords: DNA biosynthesis; nucleotidyltransferase	2.04e-186 Length: 2628.00 Matches:	Conservative Mismatches: Indels: Gaps:	US-10-761-006A-1 (1-3215) x JDVLJ1 (1-843)	OY 1 CTCCACAACATTCCACCAAGCTCTGCTAGATCCCAGGGGGGCCTATATTTTCCTGC 60	Qy 61 TGGTGGGTCCGGAACAGTAAACCCTGTTCCGACTACTGCCTCTCCCATATCGTC 120	Db 324 TrpTrpLeuGlnPheArgAsnSerLysProCysSerGluTyrCysLeuSerHislleVal 343 Ov 121 AATCTTCTCGAGGACTGCTGCACCGAACATGGAGAACATGGAGAACATGAGGATTCCT 180	:::	Oy 181 AGANCCCCGCTCGTGTTACAGGCGGGGTTTTTCTCGTTGACAGATCCTCACAATACC 240	241	384 ThrGluSerArgLeuValValAspPheSerGlnPheSerArgGlyAsnThrArgVal-Se 40	300 CIGGCCAAAATICGCAGTCCCCAACCTCCAATCACTCACCACCTCTTGTCCTCCAATITT	Db 403 rTrpProLysPheAlaValProAsnLeuGlnSerLeuThrAsnLeuSerSerAsnLe 423  Qy 360 GTCCTGGCTGGTGTGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCTTGTGCTGC 419	1 44	Qy         420 TATGCCTCATCTTGTTGGTTCTTCTGGACTACCAAGGTATGTTGCCCGTTTGTCCTC 479           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 480 TACTTCCAGGAACATCAACCACGGGGCCATGCAAGACCTGCAGGACTCCTGCTC 539	Db 463 rAsnSerArgileileAsnHisGlnHisGlyThrMetGlnAspLeuHisAsnSerCysSe 483 Ov 540 AAGGAAACTTTACGTTTTGTTGCTTTGAAAACTTCGGACGGA		600 GTATTCCCATCCTCATCTGGGGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCC	503	01111111111111111111111111111111111111	Oy 120 CTGTTTCAGTTATATAGATGATGTGGTATTGGGGGCGAAGTCTGTACAACATCT	Db 543 sCysLeuAlaPheSerTyrMetAspAspValValLeuGlyAlaLysSerValGlnHisLe 563	QY 780 IGAGICCCITITIACCICIATIACCAAITITCTITIGICITIGGGIAIACAITIAAACCC 839	Db 563	Qy 840 TAATAAAACCAAACGTTGGGGCTACTCCTTAACTTCATGGGATATTGGAAGTTG 8999	oos onsimystiitugargiipolylytoetheumsiiriiemetolylytvalliedtysetti
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900 GGGTACTTTACCGCAGGAACATATTGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC 959 	960 TGTAAATAGACCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGGTCTTTTGGGCTTTGC 1019 	1020 TGCCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATC 1079 	1080 TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAA 1139 	1140 CCTTTACCCCGTTGCCCGGCAACGGTCCGGTCTCTGCCAAGTGTTTGCTGACGCAACCCC 1199 	1200 CACTGGATGGGGCTTGGCCATCAGGCCATGGCTGGAACCTTTCTGGCTCCTCT 1259 	1260 GCCGATCCATACTGCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAA 1319 	1320 ACTTATCGGAACCGACAACTCTGTTGTCCTCTCGGAAATACACCTCCTTTCCATGGCT 1379 	1380 GCTAGGGTGCTGCCAACTGGATCCTGCGCGGGACGTCCTTTGTCTACGTCCGGTCGGC 1439 	1440 GCTGAATCCCGGGACGACCCGTCTCGGGGCCGTTTGGGGCTCTACCGTCCCCTTCTTCA 1499 	1500 TCTGCCGTTCCGGCCGACCACCACGGCGCACCTCTTTTACGCGGTCTCCCCGTATGTGCC 1559        :::	1560 TTCTCARCTGCCGGACCGTGTGCACTTCGCTTCACCTCTGCACGTCGCATGGAGACCACC 1619 	<b>ს</b> —	843 0 843
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Search completed: December 2, 2005, 00:02:30 Job time : 160 secs

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HBV; HBV surface antigen-'8'-133 Oon strain (Met to Thr); DNA polymerase; large surface antigen; core protein; transactivating X protein; hepatitis vaccine, HBV infection; hepatocellular carcinoma.
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Misc-difference 174.
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 Aay54045 Amino aci
Aap53768 Hepatitis
Aab53768 Hepatitis
Aab80043 Synthetic
Aab80958 Viral pro
Abb77789 Amino aci
Abb77789 Amino aci
Abb7787 Hepatitis
Aau37647 Hepatitis
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3320.243 Million cell updates/sec
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                                                                                                                         December 27, 2005, 20:40:32 ; Search time 180.238 Seconds
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                   - protein search, using frame_plus_n2p_modell
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1 ATGGAGAACACAACATCAGG.......
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Xgapop 10.0, Xgapext
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TrpGlyArgSerLeuTyrAsnIleLeuSerProPheLeuProLeuLeuProllePhePh 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA used in prevention of infections by hepatitis virus B - comprises structural gene of hepatitis virus adr-B surface antigen, coding gene at least 1 virus core antigen structural gene.
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354 1GINTERPHEVAIGLYLEUSERPOTHIVAITTPLEUSERVAILLETPMETHETTPTY
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                                                                                                                                                                                                         The present sequence is encoded by the genome of an isolated strain of Hepatitis B virus designated human Hepatitis B virus (HBV) surface antigen-'S--133 Oon strain (Met to Thr). The viral genome is deposited as ECCC accession numbers P97121501 and P97121503. The nucleotide sequence was isolated from hepatocellular carcinoma (HCC). The nucleotide sequence encodes four overlapping proteins, which are a DNA polymerase, a large surface antigen differs from the wild type sequence in that it contains a Thr at position 133 of the wild type sequence in that it contains a Thr at position 133 of the wild type sequence in that it contains a Thr at position 133 of the wild type sequence in that it contains a Thr at position and the used for detecting the novel HBV strain. The HBV polypeptides can be used in hepatitis vaccines. The HBV novel strain polypeptides can be used to identify compounds for treating or preventing HBV infection or hepatocellular carcinoma
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                                                                                                                                 New isolated hepatitis B virus strain, useful for, e.g. treatment hepatitis infection.
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                                                                                  WPI; 2000-106104/09.
N-PSDB; AAZ37088.
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This invention relates to a method for the preparation of a viral antigen. The method involves processing the virus antigen in the presence of a peptidyl prolyl cis-trans isomerase (PPI). Preferably a surfactant, a reducer and a protein denaturant are also added. The method is used for immune diagnosis. The present sequence represents a Hepatitis b virus protein sequence used in the invention. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                      TTTCTAGGGGGAGCACCCACGTGTTCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of viral antigen, especially hepatitis B, hepatitis C or HIV, for use as vaccine and in diagnostics, comprises reacting peptidyl prolyl cis-trans isomerase to the viral antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (M) for the preparation of a viral antigen (I) comprising reacting (I) with peptidyl prolyl cis-trans isomerase (PPIsae). (I) has virucide, antinifiammatory, anti-HIV, anti-HIV, anti-HIV, anti-HIV, anti-HIV, anti-HIV, anti-hepatitis B, antihepatitis-C and hepatotropic activities. (I) is useful for immunodiagnostics, and as a vaccine. (I) has stronger antigenic activity than previously available antigens. Large quantities of viral antigen can be prepared by the simple process within a short culture period. The present sequence represents a synthetic adr type hepatitis B surface antigen, which is given in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 TTTCTAGGGGGGGCACCCACGTGTTCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCA
                                                                                                                                                       Synthetic adr type hepatitis B surface antigen SEQ ID NO:12.
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(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
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       AAB98043 standard; protein; 226
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N-PSDB; AAH21782.
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Best Local Similarity:
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17-MAY-1999;
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The specification describes a method for preparing a recombinant hepatitis B virus (HBV) surface (HBs) antigen. The recombinant HBs antigen is useful in the preparation of immunoassay reagents. The present sequence represents a HBV protein, which was used in the course of the
                                                                                                                                                                                                                                                                                                                       TITCTAGGGGAGCACCCACGTGTTCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCA 179
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                                                                                                       surface antigen
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Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence of a hepatitis B virus (HBV) protein.
                                                                            US-10-761-006A-1_COPY_155_835 (1-681) x AAB80958 (1-226)
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hepatitis B virus surface antigen used for the preparation of immunoassay
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PheLeuGlyGlyAlaProThrCys-ProGlyGlnAsnSerGlnSerProThrSerAsnHi
                                TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTCTTCTGGACTA
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N-PSDB; ABK52589.
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             180 lGlnTrpPheValGlyLeuSerProThrValTrpLeuSerVallleTrpMetMetTrpTy
                                                          rTrpGlyProSerLeuTyrAsnIleLeuSerProPheLeuProLeuLeuProIlePhePh
TCAGTGGTTCGTAGGGCTTTCCCCCACTGTTTGGCTTTTCAGTTATAGGATGATGTGGTA
                                              TTGGGGGCGAAGTCTGTACAACATCTTGAGTCCCTTTTTTACCTCTATTACCAATTTTCTT
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delivery

antigen protein; HBsAgS; liver;

Hepatitis B virus surface antigen, HBsAgS.

Hepatitis B virus

WO2004002459-A1

(first entry)

22-APR-2004

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containing four antigen sites of the S antigen of the hepatitis B virus surface antigen and a region encoding at least four amino acids forming the membrane-penetrating region. The invention also comprises a hepatitis B virus surface antigen prepared using this method. The method of the invention is useful for the preparation of immunoassay reagents. The present sequence represents the Hepatitis B surface antigen protein #3 of the invention
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The present invention relates to a hollow nanoparticle, which comprises a protein, e.g. hepatitis B virus surface antigen protein, with modified cysteine residues. The nanoparticle specifically recognizes a target cell e.g. a liver cell. The nanoparticle is useful in methods for drug delivery. The present sequence is one such hepatitis B virus surface
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27-JUN-2003; 2003JP-00183863.
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                                   US-10-761-006A-1_COPY_155_835 (1-681) x AAR60174 (1-318)
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Japanese encephalitis virus.
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(TOKS-) TOKYOTO SHINKEI
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The present invention relates to a hollow nanoparticle, which comprises a protein, e.g. hepatitis B virus surface antigen protein, with modified eystetaine residues. The nanoparticle specifically recognizes a target cell e.g. a liver cell. The nanoparticle is useful in methods for drug delivery. The present sequence is one such hepatitis B virus surface
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                                                                                                                                                                                                                                                                                                      TTGGGGGGGGAAGTCTGTACAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTT 659
                                                                                                                                                                                   257 rGlnGlyMetLeuProValCysProLeuLeuProGlyThrSerThrThrSerThrGlyPr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hollow nanoparticle comprising protein with modified cysteine residues for target specific drug delivery.
                                                                                                                   AAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAG
                                                                                                                                                                     ATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT
                                                                                                                                                                                                                                       TCAGTGGTTCGTAGGGCTTTCCCCCCACTGTTTGGCTTTCAGTTATATGGATGATGTGGTA
                                 ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nanoparticle; surface antigen protein; HBsAgL; liver; drug delivery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus surface antigen, HBsAgL, SEQ ID 2.
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Matches:
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1206.00
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27-JUN-2003; 2003JP-00183863.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-082876/08.
N-PSDB; ADH77842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                      HBBAG L protein (P39) is an env protein. When L protein genes are introduced into animal cells (CHO cells) they produce HBBAG particles containing M and S proteins. The advantage is that peptides having HBBAG antigenicity are excreted outside the cells and easily purified. Claimed is a eukaryotic cell transformed with the rDNA. Pref. the cell is a yeast cell, sep. S. cerevisiae AH22R-/pGLD LB39-RCT, L11P39-RCT or LP31-RCT. Also claimed is recombinant DNA, which is a DNA coding for a signal peptide which functions in a eukaryotic cell, and is bound to the 5'-creminal of a DNA coding for a peptide having HBBAG activity. The signal peptide may be a signal peptide of egg white lysozme. When trypsin-like protease-producing yeast is utilized as the host, L protein and M protein can yossibly be degraded by the protease; therefore it is desirable that the genes are altered so that the 48th arginine residue from the N-terminal of M protein or a peptide containing the residue (preferably the (altered) coding for the amino acid sequence 1-383 shown in AAN80973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCAAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCATATTCCTCTTCATCCTGCTATGCCTCATCTTCTTGTTGGTTCTTCTGGACTA 299
                                                                                                                                                                                                                                                     Peptide(s) having hepatitis B surface antigenicity - used as vaccine for prevention of hepatitis B virus infection and in diagnostic kits.
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Conservative:
Mismatches:
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                                                                                                                                                                     Miyazaki T;
                                                                                                                                                                                                                                                                                                            Example; Pig 5; 31pp; English.
                                                               87JP-00098265.
87JP-00256885.
88JP-00095335.
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1206.00
96.92%
96.92%
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                                                                                                                                   (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                       WPI; 1988-301233/43.
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Best Local Similarity:
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                                 13-APR-1988;
                                                                                   12-OCT-1987;
18-APR-1988;
                                                                   20-APR-1987;
 26-OCT-1988
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                                                                         340 gPheLeuTrpGluTrpAlaSerValArgPheSerTrpLeuSerLeuLeuValProPheVa
                                                                                                                             201 LeuLeuThrArglleLeuThrlleProGlnSerLeuAspSerTrpTrpThrSerLeuAsn
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                                                                                                                TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCAAT
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                                                     x ADH77843 (1-406)
  Conservative:
Mismatches:
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Percent Similarity:
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Query Match:
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This invention relates to a novel hollow nanoparticle comprising a first protein capable of recognising specific cells and having particle forming ability, and a second protein which forms a capsid structure on the first protein. The first protein is preferably the hepatitis B virus surface antigen protein, which is capable of modifying the hepatocyte recognising site in the hepatitis B virus surface antigen protein of another biological recognition molecule, to beta cell phosphorus or a basic bibroblast growth factor (bFGF). The second protein is a hepatitis B virus inner core antigen protein. The invention is useful for treating a disease and for transferring a substance or drug specifically into a transfer of a substance or drug specifically into a transfer of a substance into a rarget cell or tissue, which can be produced in a stable yield. The present sequence is that of the Hepatitis B virus pre-SI protein gene sequence which is related to the invention.
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                                                                                                                                                                                                                                    Hollow nanoparticle, for transferring substance specifically into target cell, comprises first protein capable of recognizing specific cells e.g. hepatocyte, having particle forming ability, and second protein forming capsid structure.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                           Ueda
                                                                                                                           AGENCY
                                                                                                                                                           Kondo A,
                                                                                                                         (NISC-) JAPAN SCI & TECHNOLOGY
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1206.00
96.92%
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                                                                                                                                                           Tanizawa K,
                                                                                                                                                                                       WPI; 2004-450201/42,
N-PSDB; ADO48158.
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Best Local Similarity:
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Pred. No.:
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TTGGGGGCGAAGTCTGTACAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTT 659
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                                                                                                                                                                                                                                                61 TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCTCAAT
                                                                                                                                                                                                                                   TITCTAGGGGGGGCCCCACGTGTTCCTGGCCAAATTCGCAGTCCCCAACCTCCAATCA
                                                                                                                                                                                                                                                                                CTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATCGCTGGATGTGTCTGCGGCGTTT
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Conservative:
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                                                              Percent Similarity:
Best Local Similarity:
         Sequence 406 AA;
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                                Alignment Scores:
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           TTGGGGGGGAAGTCTGTACAACATCTTGAGTCCCTTTTTTACCTCTATTACCAATTTTCTT
ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTAC
                                                    ATTCCTATGGGAGTGGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT
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                                                                                                                                                                                                                                                                                                                                                                                  haemophilia; nanoparticle; HBV; surface antigen;
blood coagulation factor VIII; haemostatic; gene therapy
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(VIBV-) VIB VLAAMS INTERUNIVERSITAIR INST BIOTEC
(COLL-) COLLEN RES FOUND VZM ONDERWIJSEN NAVORSI
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Vandendriessche T,
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TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCAAT

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280 rGlnGlyMetLeuProValCy8ProLeuLeuProGlyThrSerThrThrSerThrGlyPr 300

CCAAGGTATGTTGCCCGTTTGTCCTCTACTTCCAGGACATCAACCACCAGCAGGGGCC

OCYSLYSTHYCYSTHY11eProAlaGInGlyThySerMetPheProSerCysCysTh

ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTAC

360

ellellePheLeuPhelleLeuLeuLeuCysLeullePheLeuLeuValLeuLeuAspTy

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The invention relates to a hollow nanoparticle (I) made of protein capable of forming particles and presents biological structure-
recognition sites on its surface, where the biological structure recognition sites are provided at both the N- and C-terminals of the recognition sites are provided at both the N- and C-terminals of the recognition sites are the following: production of (I); and sealed by (I): In (I), the biological structure recognition site with a substance and sealed by (I): In (I), the biological structure recognition site with a target. The biological structure recognition site is a target structure recognition site with recognition site is a target. The biological structure recognition site is a target. The biological structure recognition site is a target structure derived from virus e.g. hepatocyte recognition site of extructure derived from virus e.g. hepatocyte recognition site of the hepatitis B virus surface antigent protein, antigenic determinant e.g. the past structure tension site of the hepatitis B virus surface antigent protein, antigenic determinant and virus e.g. hepatocyte recognition site one or correct ag sequences are combined, or ligand e.g. cell growth factor or 22-tag. The cell growth factor is epidermal growth factor or 22-tag. The cell growth factor is epidermal growth factor or 22-tag. The cell growth factor is epidermal structure recognition site compines a tag capture and ligand protein which has particle formation ability is a surface antigen protein which has particle formation ability is a surface antigen protein. The biological structure recognition site is introduced into the cell is a compound comprising a gene compound of the proparation of the substance introduced into the cell is a compound comprising a gene compound of the proparation of the protein of the protein of the protein of the invention of the proparation of the protein of the invention of the proparation of the invention of the invention be purified efficiently and capable of forming particle and pe
                                                                                                                                                                                                                                                                                                                                                                                           Hollow nanoparticle useful in preparation of medical agent for treating disease, made of protein capable of forming particles, and presents biological structure-recognition sites on both N- and C-terminals of
                                                                                                                                                                                                                                                                               Ueda M;
                                                                                                                                                                                                                                                                               Kondo A,
                                                                                                                                                                                                                                                                            Seno M, Tada H, Kuroda S, Tanizawa K,
                                                                                                                                                                                                                               (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page; 54pp; Japanese.
                                                                                                                                      19-NOV-2004; 2004WO-JP017282,
                                                                                                                                                                                 21-NOV-2003; 2003JP-00392649
                                                                                                                                                                                                                                                                                                                        WPI; 2005-396109/40.
N-PSDB; AEA21246.
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                                             WO2005049824-A1
  Unidentified.
                                                                                           02-JUN-2005
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AAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAG

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ATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT

480 340

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TCAGTGGTTCGTAGGGCTTTCCCCCACTGTTTGGCTTTCAGTTATATGGATGATGTGGTA 599
                          380
                                                   TIGGGGGCGAAGICIGIACAACAICTIGAGICCCTITITIACCICTATIACCAATITITCTT 659
                                                              360 lGlnTrpPheValGlyLeuSerProThrValTrpLeuSerVallleTrpMetMetTrpTy
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ATGGAGAACACAACATCAGGATTCCTAGGACCCCTGCTGTTACAGGCGGGGGTTTTTC

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Length:
Matches:
Conservative:
Mismatches:
Indels:

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> Percent Similarity: Best Local Similarity:

Query Match:

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Sequence 61, Appl
Sequence 62, Appl
Sequence 56, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 63, Appl
Sequence 10, Appl
Sequence 214, Appl
Sequence 216, Appl
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Sequence 12, App]
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Chen, Wei Ning
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
ODRUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr.2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
ATIORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30.086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
US-08-591-5028-61

US-08-591-5028-62

US-08-591-5028-65

US-08-591-5028-64

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ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-10-10-20-2
; Sequence (2, Application US/09719528A
; Patent No.-6558675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Justice No. 65586, 2
GENERAL INFORMATION:
APPLICANT: Oon, Chong Jin
Lim, Gek Keow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
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2: /cgn2_6/ptCdata/1/iaa/6_COMB.pep:*
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6: /cgn2_6/ptCdata/1/iaa/RB_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                     protein search, using frame_plus_n2p model
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US-08-591-502B-48
US-08-591-502B-48
US-08-416-950-11
US-08-459-830-11
US-08-591-502B-51
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Listing first 45 summaries
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Database :

Result No.

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1201 ACTGGATGGGGCTTGGCCATAGGCCATCAGGCTGGCTGGAACCTTTCTGGCTCCTCTG 1260
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Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chong Jin
Gek Keow
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & P
STREET: 26 West 61 St
CITY: New York
STATE: New York
COUNTR: USA
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Chen, Wei Ning
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Mismatches:
Indels:
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                                                                                  Length:
Matches:
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TELEPHONE: (212) 708-1800

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
US-09-719-528A-2
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Percent Similarity:
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Query Match:
DB:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/209,264
FILING DATE: 31-Jul-2002
CLASSIPICATION: 435
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Matches:
Conservative:
Mismatches:
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FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Cliffcord J.
REGISTRATION NUMBER: 30,086
REFRENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OS 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                   GCCAAAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTCTTGTCCTCCAATTTGTC
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                                                                                                      B Virus
                                                                 APPLICANT: Chiest, Francis V.
AITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                              NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
TELEFANE: (415) 576-0200
TELEFANE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 01-AUG-1994
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/591,502B
FILING DATE: 20-May-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid

STRANDEDNESS: «Unknown»

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-08-591-5028-45
RESULT 3
US-08-591-502B-45
; Sequence 45, Application US/08591502B
; Patent No. 6607727
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 843 amino acids
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                      TATCGGAACCGACACACTCTCTCTCTCGGAAATACACCTCTCTTCCATGGCTGCT
                                                                        AGGGTGTGCTGCCAACTGCATCCTGCGCGGACGTCCTTTGTCTACGTCCGGTCGGCGCT
                                                                                                                                                                                                                                                                                          Sequence 59, Application US/08591502B
Patent No. 6607127
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 02-AUG-1993
ATPLING DATE: 01-AUG-1994
ATTORNEY/AGENT NUMBER: UN PCT/US94/08685
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-591-5028-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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STRANDEDNESS: <Unknown>
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US-08-591-502B-59
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843
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          Matches:
Conservative:
Mismatches:
Indels:
                                                                                US-10-761-006A-1 (1-3215) x US-08-591-502B-59 (1-843)
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                                                                                                                                                                                              NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; 
; MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-591-502B-47
                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 47:
                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                              LENGTH: 843 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.75e-246
2788.00
97.97%
96.67%
47.20%
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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Best Local Similarity:
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                                                                                            TGCCCCTTTTACACAATGTGGCTATCCTGCCTTGATGCCTTTATATGCATGTATACAATC
                                                                                                               pGlyThrLeuProGlnGluHisIleValGlnLysLeuLysGlnCysPheArgLysLeuPr
                                                                                                                                                          TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAA
                                                                                                                                                                                                                          CCTTTACCCCGTTGCCCGGCAACGGTCCCGGTCTTGCCAAGTGTTTGCTGACGCAACCCC
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                                                     OVALASRAXGProlleAspTrpLysValCysGlnArglleValGlyLeuLeuGlyPheAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPANIE NEADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,502B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-51-502B-47
US-08-51-502B-47
Sequence 47, Application US/08591502B
Patent No. 6607727
GENERAL INFORMATION
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CTCCACACATTCCACCAAGCTCTGCTAGATCCCAGGGTGAGGGGCCTATATTTTCCTGC
                                                                                               Sequence 46, Application US/08591502B

Patent No. 6607727

GENERAL INFORMATION: Peptides for Inducing Cytotoxic T

TITLE OF INVENTION: Peptides for Inducing Cytotoxic T

Lymphocyte Responses to Hepatitis B Virus

NUMBER OF SEQUENCES: 99

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LIP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                  COUNTY: USA

ZIP: 94111-1834

COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIDLE
COMPUTER: IBM PC COMPALIDLE
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
RELING DATE: 20-May-1996
CLASSIFICATION: <Unknown>
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REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540

RILING DATE: 26-AUG-1991

APPLICATION NUMBER: US 07/935,898

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 08/100,870

FILING DATE: 02-AUG-1993

APPLICATION NUMBER: US 08/100,870

FILING DATE: 02-AUG-1993

APPLICATION NUMBER: US 08/100,870

FILING DATE: 01-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 845 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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97.04%
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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Best Local Similarity:
1620 G 1620
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                                                                     RESULT 6
US-08-591-502B-46
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                                                                                         TTCCTATGGGAGTGGGCCTCAGTCC
                                                                                                                                                             GTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCCA
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TCTGCCGTTCCGGCCGACGGGGGGCGCACCTCTTTACGCGGTCTCCCCGTATGTGCC 1559
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Sequence 11, Application US/08416950

Patent No. 5780036

Patent No. 5780036

Patent INFORMATION:

APPLICANT: CHISARI, Francis V.

TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T

TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                        NO: 48
 REFERENCE/DOCKET NUMBER: 014

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 amino acids
TYPE: amino acid STRANDEDNESS: <UNKNOWN>
TYPE: amino acid STRANDEDNESS: <UNKNOWN>
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: US-08-591-5028-48
                                                                                                                                            1.25e-243
2759.00
97.23%
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Matches:
Conservative:
Mismatches:
Indels:
                                                    COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARTICULATION DATA:
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,950
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: PARMELE NUMBER: 31,990
REGISTRATION NUMBER: 
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SEE: Townsend and Townsend Khourie
: One Market Plaza, Steuart Street
San Francisco
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MOLECULE TYPE: peptide
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Best Local Similarity:
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                                                                            ABnLeuLeuGluAapTrpGlyProCysThrGluHisGlyGluHisAsnIleArgllePro
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                                             121 AATCTTCTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATCAGGATTCCT
                                                                                                  AGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTCGTTGACAAGAATCCTCACAATACC
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Matches:
Conservative:
Mismatches:
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                                                                                                                                 Sequence 11, Application US/08469830 Patent No. 5932224
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2759.00
97.23$
95.38$
46.71$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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Query Match:
DB:
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US-08-469-830-11
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346 AsnLeuLeuGluAspTrpGlyProCysThrGluHisGlyGluHis***11eArg11ePro 365
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                              NAME: Weber, Bilen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 845 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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Matches:
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US-08-591-502B-11
                                                                                                                                                                                                                                                                                                LOCATION: 1..845
OTHER INFORMATION: /product=
/note= "Xaa = any amino acid
(<50% consensus)"
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   FILING DATE: 01-AUG-19
ATTORNEY/AGENT INFORMATION:
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2741.00
96.30%
95.01%
46.40%
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Best Local Similarity:
Query Match:
DB:
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                                                                                       nLeuTyrProvalAlaArgGlnArgProGlyLeuCysGlnValPheAlaAspAlaThrPr
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TAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCTGTGTAAACAATATCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08591502B
Patent No. 6607727
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 9411.389
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/591,502B
FILING DATE: 20-May-1996
CLASSIFICATION: cUnknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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RESULT 14
US-08-591-502B-51
is Gequence 51, Application US/08591502B
is Sequence 51, Application US/08591502B
is GENERAL INCRMATION:
is GENERAL INCRMATION:
is TIPLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

WEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US 08/591,502B
FILING DATE: 20-May-1996
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1993
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 01-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Righth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELEPHONE: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 842 amino acids
TYPER: TYPER:
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Matches:
Conservative:
Mismatches:
Indels:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-591-502B-51
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US-08-591-502B-61
Sequence 61, Application US/08591502B
Sequence 61, Application US/08591502B
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Sequence 61, Application US/08591502B
SEQUENCE 61, MANATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Dymphocyte Responses to Hepatitis B Vi
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREES: Townsend and Townsend and Crew LLP
STREES: Townsend and Townsend and Crew LLP
STREES: ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESS TOWNSENDER CONTRY: USA
CITY: San Francisco
STATE: California
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Matches:
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Mismatches:
Indels:
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID
US-08-591-5028-50
                                                              6.28e-241
2729.50
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Best Local Similarity:
Query Match:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIV APPLICATION DATA:
APPLICATION NUMBER: US/08/591,502B
FILING DATE: 20-May-1996
CLASSIPICATION: «Unknown»
PRIOR APPLICATION OF THE OF T
                                                                                                                                                                                                                                                              MAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION: DOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-08-591-502B-61
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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Query Match:
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                                                                 RESULT 14
US-08-591-502B-62
; Sequence 62, Application US/08591502B
; Patent No. 6607027;
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis F
                                                                                                                                                                                                         ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                          NUMBER OF SEQUENCES: 99 CORRESPONDENCE ADDRESS: POCRRESPONDENCE ADDRESS: STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
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495
119
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REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
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ULE TYPE: protein
NCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 832 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
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2646.00
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91.50%
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                                                                                                                                                                                                  COUNTRY: USA
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Best Local Similarity:
Query Match:
DB:
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SEQUENCE
US-08-591-502B-62
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Pred. No.:
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Matches:
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                                                                                                                                                                         NO.
                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 843 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: linear
WOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 56:
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95.19%
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Patent No. 660727
GENERAL INFORMATION:
APPLICANT: Chieari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
NUMBER OF SEQUENCES: 99
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/591,5028
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ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weber, Ellen Lauwer
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-MAY-1996
CLASSIFICATION: UNKnown>
CLASSIFICATION: UNknown>
IOR APPLICATION DATE:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 08/100,870
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: US 08/100,870
FILING DATE: 01-AUG-1993
FILING DATE: 01-AUG-1994
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Run on:

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Sequence:

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HBV; HBV surface antigen-'8'-133 Oon strain (Wet to Thr); DNA polymerase; large surface antigen; core protein; transactivating X protein; hepatitis vaccine, HBV infection; hepatocellular carcinoma.
                                                                                                                                                 Aea08851 Hepatitis
Aea08850 Hepatitis
Adx40740 HBV polym
Adx40770 HBV polym
Aay54045 Amino aci
Aea0832 Hepatitis
Aap60560 Hepatitis
Aap60560 Hepatitis
Aap70294 Subtype a
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Aar970294 Hepatitis
Adr74394 HBV S-pro
Adr49718 Hepatitis
Adr74394 HBV S-pro
Adr49718 Hepatitis
Aar62870 Hepatitis
Amino acid segeunce of a HBV DNA polymerase protein.
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          Misc-difference 194
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                       protein search, Weing Erame plus n2p model
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Listing first 45 summaries
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The present sequence is encoded by the genome of an isolated strain of antigen-'8'-130 on strain (Met to Thr). The viral genome is deposited as antigen-'8'-130 on strain (Met to Thr). The viral genome is deposited as ECCC accession numbers P97121501, P97121502 and P97121503. The nucleotide sequence was isolated from hepatocellular carcinoma (HCC). The nucleotide sequence encodes four overlapping proteins, which are a DNA polymerase, a large surface antigen, a core protein, and a transactivating X protein. The large surface antigen differs from the wild type sequence instead of a Met. The proteins are used to produce antibodies. The proteins, polymucleotide and antibodies can be used for detecting the novel HBV strain. The HBV polypeptides can also be used in hepatitis vaccines. The HBV novel strain polypeptides can be used to identify compounds for treating or preventing HBV infection or hepatocellular carcinoma
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                                                treatment
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                                                                              Disclosure; Page 36-39; 68pp; English
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RESULT 2 ADX40768

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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope. Comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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Disclosure; Page 380-385; 458pp; English.
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enzyme

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Hepatitis B virus

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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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used, particularly ex vivo, to stimulate CTL cells. These cells can be reintroduced into patients who have chronic or acute HBV infections or are carriers, especially in treatments to prevent conversion from acute to chronic infections. (Updated on 25-MAR-2003 to correct PN field.)
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RESU ADX4 ID	ULT 8 40775 ADX40775 standard; protein; 843 AA.
¥ 2	ADX40775;
XE:	21-APR-2005 (first entry)
ž B Š	HBV polymerase protein #18.
{₫;	Immune stimulation; polymerase; enzyme.
<b>88</b> 3	Hepatitis B virus.
{ <b>&amp;</b> }	WO2005012502-A2.
<b>\$ &amp;</b>	10-FEB-2005.

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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an

Disclosure; Page 380-385; 458pp; English.

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infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HBV polymerase protein used in the scope of the invention.
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                                                                                                                                            eArgProThrThrGlyArgThrSerLeuTyrAlaValSerProSerValProSerHieLe
                                                                                   SAlaAlaAsnTrplleLeuArgGlyThrSerPheValTyrValProSerAlaLeuAsnPr
AACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTCCATGGCTGCTAGGGTG
                TECTECCAACTGGATCCTGCGCGGGACGTCCTTTGTCTACGTCCCGGTCGGCGCTCGAATCC
                                                                                                                               CGCGGACGACCCGTCTCGGGGCCGTTTGGGGCTCTACCGTCCCCTTCTTCATCTGCCGTT
                                                                                                                                                                                             CCGGCCGACCACGGGCGCCTCTTTACGCGGTCTCCCCGTATGTGCCTTCTCATCT
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Rossau R;
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HBX; HBPol; HBeAg.

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                       TGTAAATAGACCTATTGATTGGAAAGTATGTCAAAGAATTGTGGGGTCTTTGGGGCTTTTGC
                                                                              aAlaProPheThrGlnCysGlyTyrProAlaLeuMetProLeuTyrAlaCysIleGlnAl
                                                                                                                            CCTTTACCCCGTTGCCCGGCAACGGTCCCGGTCTTGCCAAGTGTTTGCTGACGCAACCCC
                                                                                                                                   CACTGGATGGGCCTTGGCCATAGGCCATCAGCGCATGGCTGGAACCTTTCTGGCTCCTCT
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                GGGTACTTTACCGCAGGAACATATTGTACTAAAACTCAAGCAATGTTTTCGAAAACTGCC
                                                 Hepatitis B virus; HBV; preCore; Core; preS1; preS2; HBS;
HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg;
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by HBV genotype G. The present sequence is 1 FR1, genotype G polymerase protein, HBpol
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stage of liver disease caused b
hepatitis B virus (HBV) strain
                                        1.06e-203
2675.00
96.30%
91.68%
45.29%
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The invention relates to the complete nucleic acid sequence of a new human hepatitis B virus (HBV) genotype, provisionally named genotype G. This genotype was found with a high prevalence in patients chronically infected with HBV and residing in Europe and the USA. The invention relates to a fully defined sequence of 3248 nucleotides as given in specification, a sequence with 92* identity to the given sequence, or sequence that is degenerate to the mentioned sequences. These polymucleotides are useful for HBV genotyping. The proteins encoded by the polymucleotides are useful for detecting antibodies in a biological sample. Ligands that bind to the proteins and antibodies directed against the protein are useful for detecting the proteins and for detecting proteins and HBOAg (precove precursor proteins). They are also useful for preparing a vaccine or medicament for treating HBV infections. The present sequence is encoded by the genome of HBV genotype G strain FRI
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Conservative: Mismatches: Indels: Gaps:

Similarity:

Query Match:

large surface anti major surface anti

Best Local

Percent Similarity:

surface antigen -surface antigen -

Result No.

surface antigen -

surface antigen surface antigen

US-10-761-006A-1\_COPY\_527\_595 (1-69) x JQ2054 (1-226)

Sequence:

Perfect

Run on:

Searched:

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UG2054

Burface antigen - hepatitis B virus (subtype indet, strain Tar)

C,Species: hepatitis B virus, HBV

C,Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004

C,Accession: JQ2054; PQ0571

C,Accession: JQ2054; PQ0571

A,Norder, H.; Hammas, B.(Tiep-S,D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius J. Gen. Virol. 74, 1341-1348, 1993

A,Title: Genetic relatedness OF Hepatitis B viral strains of diverse geographical original A,Contents: genogroup A

A,Accession: JQ2054

A,Accession: JQ2054
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A; MOLOCULE UPPE: DNA
A; MOLOCULE UPPE: DNA
A; CTOSE-references: 1-226 <NORN-
A; CTOSE-references: UNIPROT: QBJURP7; UNIPROT: Q9Q3D4; UNIPROT: QBJUKH6; UNIPROT: O41759; UNI
PROT: O41755; UNIPROT: O41746; UNIPROT: Q91042; UNIPROT: Q91042; UNIPROT: Q910424; UNIPROT: Q910424; UNIPROT: Q910427; UNIP
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Matches:
                     SAVLVD
JQ1574
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JQ2101
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                                                                                                 Alignment Scores:
Pred. No.:
-MODEL: frame + n2p.model - DEVexlp
-Q=/cgn2_1/USPTO_epool_p/US10761006/runat_27122005_192901_15763/app_query.fasta_1.1102
-Q=/cgn2_1/USPTO_epool_p/US10761006/runat_27122005_192901_15763/app_query.fasta_1.1102
-DB=-IR -OFMT=fastan -SUPFIX=rpr -MINMARCH=0.1 -LOOPCIA=0 -LLOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINS=0 -ALIGN=15 -MODE=LOCAL
-USRR=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USRRS-US10761006 @CCR 1 1 77 @cunat_27122005 192901 15763 -NCPU=6 -ICPU=3
-NO MMAP -LARGRQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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2: pir2:*
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JT0293
K;Ivivian, M.B.; Lunin, V.G.; Mahov, A.M.; Tikchonenko, T.I.; Kukain, R.A.
Gene 64, 285-286, 1988
A;Title: Nucleotide sequence of integrated hepatitis B virus DNA and human flanking regi
A;Reference number: JT0293; MUID:88297159; PMID:2841200
A;Accession: JT0293
A;Molecule type: DNA
A;Residues: 1-226 <RIV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Surface antigen - hepatitis B virus (subtype adw2, strain 8903/86)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: UQ2052
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: UQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup A
A;Accession: UQ2052
                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P31873; UNIPARC:UPI00001389B6; GB:M21030; NID:g329702; PIDN:
C;Genetics:
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S.Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;3/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q9W7W6; UNIPARC:UPI00000FA191
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Gaps:
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145 GlyAsnCys 147
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145 GlyAsnCys 147
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001577

001577

001578cies hepatitis B virus, HBV

A.Note: host Hemo sapiens (man)

C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C.Accession: U01577; J02049; F00071

J. Gen. Virol. 73, 1201-1204, 1992

A.Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis

A.Reference number: J01577

A.Reference number: U01577 MID: 92268879; PMID: 1588323

A.Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis

A.Accession: U01577

A.Reference number: J01577

A.Reference number: J226 AND: A. J. Ball. J44, 1341-1344, 1933

A.Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin

A.Reference number: J02044; MUID: 93329382; PMID: 8336122

A.Reference number: J226 AND: A.Reference number: D01573

A.Reference number: P00453; MUID: 93107848; PMID: 1469553

A.Reference number: P00573

A.Reference
                                                         125 ThrThrProAlaGlnGlyAsnSerWetPheProSerCysCysTyrLysProThrAsp 144
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                              1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACTTTCGGAC
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C,Superfamily: hepatitis B virus surface antigen
C,Keywords: glycoprotein; surface antigen
F;3/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
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145 GlyAsnCys 147
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145 GlyAsnCys 147
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Surface antigen - hepatitis B virus (subtype aywl, strain Bat)
C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Species: Jo3-feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: J02048
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius B, J. Gen. Virol. 74, 1341-1348, 1993
A;Tile: Genetic relatedness of hepatitis B viral strains of diverse geographical origi. A;Reference number: J02044; MUID: 93329382; PMID: 8336122
A;Contents: genogroup A
A;Contents: genogroup A
A;Accession: J02048
A;Accession: J02048
A;Residues: 1-226 *NORA
A;Residues: 1-226 *NORA
A;Cross-references: UNIPROT: Q9DLM8; UNIPROT: Q9QAM3; UNIPROT: Q9SJWP7; UNIPROT: Q9JJA4; UNIPROT: Q9JJK43; UNIPROT: Q9JJK43; UNIPROT: Q9JJK42; UNIPROT: Q9JJK43; UNIPROT: Q9JJK42; UNIPROT: Q9JJK42; UNIPROT: Q9JJK43; UNIPROT: Q9JJK44; UNIPROT: Q9JJK44; UNIPROT: Q9JJK44; UNIPROT: Q9JJK44; UNIP
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A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origi A;Reference number: JQ2044; MUID:93329382; PMID:8336122
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C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: JQ2055
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145 GlyAsnCys 147
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C,Keywords: surface antigen
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145 GlyAenCye 147
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A, Molecule type: DNA
A, Residues: 1-226 <NOR>
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A; Residues: 1-226 <NOR>
A; Residues: 1-226 <NOR>
A; Cross-r-references: UNIPROT: 091938; UNIPROT: Q9EGUO; UNIPROT: Q9YVD6; UNIPROT: Q8JWP7; UNIFPOT: Q9YVD5; UNIPROT: 041755; UNIPROT: 041746; UNIPROT: 090565; UNIPROT: 041744; UNIPROT: 090787; UNIPROT: Q9JXHO; UNIPROT: Q8JXHO; UNIPROT: Q8JXHO; UNIPROT: Q8JXHO; UNIPROT: Q9JC42; UNIPROT: Q8JLK7; UNIPROT: Q8JL
                      Gurface antigen - hepatitis B virus (subtype adw2, strain 3138/87)
C;Species: hepatitis B virus, HBV
C;Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession. JQ2063.
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup A
A;Accession: JQ2053
                                                                                                                                                                                                                                                                                                                                                                                                                                           A, MOJECULE TYPE: DNA
A, ROBIGULE TYPE: DNA
A, REBIGUES: 1-226 <NOR>
A, REBIGUES: 1-226 <NOR>
A, CTOSS-references: UNIPROT: Q9DLM8; UNIPROT: Q9QAM3; UNIPROT: Q8JMP7; UNIPROT: Q9G3D4; UNIF
A, CTOSS-references: UNIPROT: Q41755; UNIPROT: Q41746; UNIPROT: Q910863; UNIPROT: Q8JXH0; UNIPROT: Q91LG42; UNIPROT: Q8JXH0; UNIPROT: Q91LG7; UNIPROT: Q8JXH0; UNIPROT: Q91LG7; UNIPROT: Q91LG7;
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Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Vivol. 14, 11340, 1993
A; Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A; Reference number: JQ2044; MUD:93329382; PMID:8336122
A; Contents: genogroup A
A; Accession: JQ2050
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C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
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Best Local Similarity:
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Surface antigen - hepatitis B virus (subtype adw2, strain Len)
C,Species: hepatitis B virus, HBV
C,Species: hepatitis B virus, HBV
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C,Accession 102045
R,Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
J. Gen. Virol. 74, 1341-1348, 1993
J. Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A,Reference number: JQ2044; MUID:93329382; PMID:8336122
A,Contents: genogroup A
A,Accession: JQ2045
A,Molecule type: DNA
A,Residues: 1-226 <NOR>
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PROT:039886; UNIPROT:041754; UNIPROT:041758; UNIPROT:042029; UNIPROT:Q9TVD5; UNIPROT:Q91C42; UNIPROT:Q9JLX2; UN
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C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
B;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: 042044; MUID:93329382; PMID:8336122
A;Cotession: 042056
A;Molecule type: DNA
A;Residues: 1-226 <NOR>A;Molecule type: DNA
A;Cross-references: UNIPROT:Q81185; UNIPROT:Q81184; UNIPARC:UPI0000178449
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                                                              1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
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  x JQ2046 (1-226)
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145 GlyAsnCys 147
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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J. Generic relatedness of hepatitis B viral strains of diverse geographical origin A; Reference number: J02044; MUID:93329382; PMID:8336122
J. Contents: genogroup A
J. Contents: genogroup A
J. Contents: genogroup A
J. Residues: 1-226 AND
J. Residues: 1-226 AND
J. Residues: 1-226 AND
J. Residues: 1-226 AND
J. CONTENTS: JOHNEOT: Q9103C9; UNIPROT: Q913C9; UNIPROT: Q910C42; UNIP
                                                                                                                                                                                                                                                                                                                                         Cyaccession: J02078
R; Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. General Brands, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. General Brands, B.; Lee, S.D.; Bile, K.; Couronce, A.M.; Mushahwar, I.K.; Magnius, J. General General General Brands of hepatitis B viral strains of diverse geographical origin A; Reference number: J02044; MUID:93329382; PMID:8336122
A; Contents: geographical origin A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-226 cNOR>
A; Cross-references: UNIPROT:Q67886; UNIPARC:UPI0000178428
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C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: JQ2046
                                                                                                                                                                                                                                               surface antigen - hepatitis B virus (subtype ayw, strain aywmut)
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: JQ2078
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Matches:
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145 GlyAsnCys 147
                                                                                                                                      145 GlyAsnCys 147
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A,Residues: 175-400 «NOR»
A,Cross-references: UNIPARC:UPI0000002E4; GB:X75666; NID:g416074; PIDN:CAA53362.1; PID
A,Experimental source: subtype adw2, strain P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ajintrons: 122/3

CjSuperfamily: hepatitis B virus surface antigen
CjSuperfamily: hepatitis B virus surface antigen
CjSuperdas: glycoprotein; surface antigen
Fj1-400/Product: surface antigen pre-Si (large envelope protein) #status predicted <PS1
Fj1-119/Domain: pre-Si domain #status predicted <PRE1>
Fj10-140/Product: surface antigen pre-Si (middle envelope protein) #status predicted <PS1
Fj10-140/Pomain: pre-Si domain #status predicted <PRE2>
Fj17-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>
Fj17-Honding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                      A; Molecule type: DNA
A; Residues: 1-400 < PLUI>
A; Residues: 1-400 < PLUI>
A; Cross-references: UNIPROT: Q67896; UNIPARC: UPI00000F5BAF; EMBL: Z35717; NID: g527440; PI: A; Cross-references: UDLYpe adw2
A; Experimental source: subtype adw2
R; Norder, H.; Hammas, B.; Loefdahl, S.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
                               polish isola
                                                                                                                                                                                                                                                                               A,Title: Comparison of the amino acid sequences of nine different serotypes of A; Reference number: JQ1570; MUID:92268879; PMID:1588323 A;Accession: JQ1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      large surface antigen - hepatitis B virus (subtype adw, strain 991)
N;Contains: major surface antigen; middle surface antigen
C;Species: hepatitis B virus, HBV
C;Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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C;Keywords: glycoprotein; surface antigen
F;120-400/Product: middle surface antigen (gene pre-2/S) #status predicted ·
F;175-400/Product: major surface antigen (gene S) #status predicted «MSA»
F;15,123,177/Binding site: carbohydrate (Asn) (covalent) #status predicted
submitted to the EMBL Data Library, August 1994
A;Description: Molecular cloning and sequencing of two complete genomes of
A;Reference number: 847404
A;Accession: 847411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
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A;Residues: 1-400 <KOE>
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A; Residues: 1-389 <0NO>
A; Cross-rences: UNIPROT: P03142; UNIPARC: UPI00001389C4; GB: V00866; GB: J02201
A; Cross-rences: UNIPROT: P03142; UNIPARC: UPI00001389C4; GB: V00866; GB: J02201
B; Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
J. Gen. Virol. 74, 1341-1348, 1993
A; Title: Genteic relatedness of hepatitis B viral strains of diverse geographical origin
A; Reference number: J02044; MUID: 93329382; PMID: 8336122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; subtype
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NyAlternate names: envelope protein; HBs antigen
NyContains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2
C;Species: hepatitis B virus, HBV
A;Variety: subtype adw2
C;bate: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: 847411; JQ1575
R;Plucienniczak, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: pre-S1/pre-S2/S
C;Superfamily: hepatitis B virus surface antigen
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F;4,26,112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted
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N;Contains: major surface antigen; middle surface antigen
C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A93460; JQ2044; A93706
R;Ono, Y:; Onda, H:; Sasada, R:; Igarashi, K.; Sugino, Y:; Nishioka, K.
Nucleic Acids Res. 11, 1747-1757, 1983
A;Title: The complete nucleotide sequences of the cloned hepatitis B virus D
A;Reference number: A93460; MUID:83168919; PMID:6300776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: genogroup A, subtype adw2, strain pHBV933
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A, Cross-references: UNIPARC:UP10000156BE0
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STRAIN=FWU005;
Lin X., Zheng D.L., Xu X.;
Lin X., Zheng D.L., Xu X.;
Submitted (DEC-2002)= Control of Control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186C43D550FB8DAA CRC64;
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Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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Matches:
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0958617 HPBNO
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Q80H30;
    Pfam; PF00695; vMSA; 1.
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-Q=/Cgn2_1/USPTO spool_p/US10761006/runat_27122005_192900_15751/app_query.fasta_1.1102
-Q=/Cgn2_1/USPTO spool_p/US10761006/runat_27122005_192900_15751/app_query.fasta_1.1102
-Q=/Cgn2_1/USPTO spool_p/US10761006/runat_27122005_1000FLG=0.LOOPECT=0.LOOPET=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USRET=bct -TRANSECTES=500 -MINLEN=0 -MAXLEN=2000000000
-USRE=SCH_TRANSECTEST -NEG SCORES=0 -MAIT_-DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE=6 -DELEXT=7
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                                                                                                                                                           December 27, 2005, 20:41:12; Search time 23.046 Seconds (without alignments) 4224.720 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                  ......AACCTTCGGACGGAACTGC 69
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Kgapop 10.0, Kgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Length:
Matches:
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Gaps:

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299 ThrThrProAlaGlnGlyAsnSerThrPheProSerCysCysCysThrLysProSerAsp 318
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                                           400 AA; 43741 MW; DIDFC54CDF11FA91 CRC64;
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                                                                                              1.34e-13
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       Pfam; PF00695; vMSA; 1.
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GlyAsnCys 35
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                   Percent Similarity:
Best Local Similarity:
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"Full-length genomic analysis of hepatitis B virus isolates in a gatient progressing from hepatitis to hepatocellular carcinoma.";
J. Med. Virol. 64:299-304(2001).
EMBL; AF182804; AAG16950.1; -; Genomic_DNA.
PIR; JQ2094; JQ2094.
PIR; JQ2112; JQ2112.
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_surfAg.
                                                                                                                                                                                                                                                                                       [1]
NUCLEOTIDE SEQUENCE.
STRAIN=WLAP10;
MEDLINE=21361487; PubMed=11468748; DOI=10.1002/jmv.1050;
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STRAIN-EMUOOS, and FWUOOB;
Lin X., Zheng D.L., Xu X, Zheng D.L., Xu X, Zheng D.L., Xu X, Zheng D.E., Xu X, Zheng D.E., Xu X, Zheng D.S., Xu X, Zheng D.S., Yu X, Zheng D.S., Yu X, Zheng X, Yu X, Y
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Orthohepadnavirus.
NCBI_TaxID=10407;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Large S protein.
Viruses; Retro-transcribing viruses; Hepadmaviridae;
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25, Surface protein. Hepatitis B virus.
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139.00
100.00%
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Q9E8K9;
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080515;
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145 GlyAsnCys 147
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SEQUENCE
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DB:
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1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
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                                                                                                                                                                                                                                                                                       Another States and Hepatitis C Virus (HCV) or Hepatitis D Virus (HDV) in Blood Domors, Patients with Chronic Liver Disease and Patients on Hemodialysis in Strabaya, Indonesia."; Microbiol. Immunol. 47:969-975.[2003].

EMBL, AB113296; BAC99010.1; -; Genomic DNA. Go, Go.0106032; Pavieral life cycle; IEA. InterPro; IPR00349; Hepvir_surfAg.

PATHRIOS23; Hepvir_surfAg.

PATHRIOS25; WASA; 1.
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                                                                                                                                                    Viruses, Retro-transcribing viruses, Hepadnaviridae, Orthobepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A8B0FB021386382C CRC64;
                                         05-071-2004 (TrEMBLrel. 27, Created)
05-071-2004 (TrEMBLrel. 27, Last sequence update)
05-071-2004 (TrEMBLrel. 27, Last annotation update)
Surface antigen (Fragment).
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Mismatches:
Indels:
71 AA
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Matches:
PRT;
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71 71
71 AA; 7861 MW;
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100.00%
95.65%
Q767N5_HPBV0 PRELIMINARY;
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98 98
98 AA; 11040 MW;
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MEDLINE=98449868; PubMed=9774595;
MEDLINE=98449868; PubMed=9774595;
MEDLINE=98449868; PubMed=9774595;
MEDLINE=98449868; PubMed=9774595;
MEDLINE-1 C., Campos R.;
Todiatric populations from Argentina.";
Todiatric populations from Argentina.";
L. J. Clin. Microbiol. 36:3362-3365(1998).

REMBL; AP043576; AAC79977.1; -; Genomic_DNA.
GO; OC:0016032; Prival life cycle; IEA.
RILTEPERO; IPR000349; Hepvir_surfAg.
RANTHER; PTHR10832; Hepvir_surfAg.
PFam; PP00695; VMSA; 1.
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Orthohepadnavirus.
NCBI_TaxID=10407;
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71 AA; 7847 MW; B94A1002139B353C CRC64;
                                                                    01-NAY-1999 (TrEMBLrel. 10, Created)
01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Surface antigen (Fragment).
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ID GOCKTE HPBVO PRELIMINARY;

DT 01-MAY-2000 (TrEMBLEE] 13, Cr

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NCBI_TaxID=10407;
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ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTTGTTGCTTGTACAAAACCTTCGGAC 60
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Weinberger K.M., Bauer T., Boehm S., Jilg W.;
"High genetic variability of the group-specific a-determinant of
hepatitis B virus surface antigen (HBBAg) and the corresponding
fragment of the viral polymerase in chronic virus carriers lacking
detectable HBBAg in serum.";
J. Gen. Virol. 0:0-0(2001)
EMBL; AF209403; AAF23486.1; -; Genomic_DNA.
GO; CO:0016032; P:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_surfAg.
PANTHER; PTHR10812; Hepvir_surfAg;
PEANTHER; PTHR10812; Hepvir_surfAg;
PEANTHER; PTHR10812; Hepvir_surfAg;
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09E458DE7C0BB075 CRC64;
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Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23,
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145 GlyAsnCys 147
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145 GlyAsnCys 147
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WICLINE-22652772; PubMed=12767980;

MEDLINE-22652772; PubMed=12767980;

MEDLINE-22652772; PubMed=12767980;

MEDLINE-22652772; PubMed=12767980;

MEDLINE-22652772; PubMed=12767980;

Parekh S., Zoulim F., Ahn S.,

Trepo C., Wands J., Tong S.;

Trepo C., Wands J., Hepvir SurfAg;

Trepo C., Wands J., Hepvir SurfAg;

PROMITER: PTHR10832; Hepvir SurfAg;

Trepo C., Wands J., Wands 
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BELLINE-2027988; PubMed=10796895; DOI=10.1053/he.2000.6407;

Ireland J.H., O'Donnell B., Basuni A.A., Kean J.D., Wallace L.A.,

Lau G.K.K., Carman W.F.;

"Reactivity of 13 in vitro expressed hepatitis B surface antigen
variants in 7 commercial diagnostic assays.";

Hepatology 31:1176-1182(2000).
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STRAIN=SA4;
Ireland J., Kean J., O'Donnell B., Basuni A.A., Wallace L.A.,
Carman W.F., Lau G.K.K.;
Submitted (MAR.1999) to the EWBL/GenBank/DDBJ databases.
EMBL, AF134144; AAD31861.1; -; Genomic_DNA.
PIR; JQ2045; JQ2045.
PIR; JQ2049; JQ2044.
PIR; JQ2048; JQ2048.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 25, Last annotation update)
Surface antigen.
Hepatitis B virus.
Viruses, Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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                                                                                                                    Viruses, Retro-transcribing viruses, Hepadnaviridae, Orthohepadnavirus.

ORDI_TaxID=10407;
     01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Mismatches:
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Q9WHS1;
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145 GlyAsnCys 147
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Best Local Similarity:
Query Match:
DB:
                                                                                                Hepatitis B virus.
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                                                       protein.
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Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Matches:
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Matches:
PIR; JQ2050; JQ2050.

PIR; JQ2051; JQ2051.

PIR; JQ2053; JQ2053.

PIR; JQ2054; JQ2054.

GO; GO:0016032; Prviral life cycle; IEA.

InterPro; IPR000349; Hepvir_surfag.

PANTHER; PTHR10832; Hepvir_surfag. 1.
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Best Local Similarity:
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MUCLECTIDE SEQUENCE.

MEDLINE=22552772; PubMed=12757980;

X MEDLINE=22552772; PubMed=12757980;

A Trepo C., Wands U., Tong S.;

Trepo C., Wands U., Tong S.;

Trepo C., Wands U., Tong S.;

Tadenome replication, virion secretion, and e antigen expression of naturally occurring hepatitis B virus core promoter mutants.";

J. Virol. 77:6601-6612(2003).

ME RMBL; APS37372; AANIS127.1; -; Genomic_DNA.

ROO:0016032; P:viral life cycle; IRA.

InterPro; IPR000349; Hepvir_surfAg.

ROO:0016032; P:viral life cycle; IRA.
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SEQUENCE 400 AA; 43651 MW; 6E6C6630699CC81E CRC64;
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Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Surface antigen (Fragment).
Hepatitis B virus.
                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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ID Q9QSL7_HPBV0_PRELIMINARY;
AC Q9QSL7;
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Q8BCB3;
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Best Local Similarity:
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1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
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Production.",

EMBL, 875184; AAP31568.1; -; Genomic_DNA.

GO; GO:0016032; P:viral life cycle; IEA.

InterPro; IPR00349; Hepvir_surfAg.

PANTHER; PTHR10832; Hepvir_surfAg.

PANTHER; PTHR10832; VASA; 1.
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MEDLINE-95154763; PubMed-7851832;
Moriyama K., Takada T., Teutsumi Y., Pukada K., Ishibashi H., Niho Y.,
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63 AA, 6826 MW, D7390D121BEB1738 CRC64;
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QBOBT7;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OUT-2003 (TrEMBLrel. 25, Last annotation update)
$ protein.
Hepatitis B virus.
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AC QODUJA;
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Query Match:
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OGUATA Y., KULCOGAKI M., Asahina Y., Enomoto N., Marumo F., Sato C.;

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

REMEL, BAR02963; BAR20346.1; -; Genomic_DNA.

PIR, JQ2094; JQ2094.

PIR, JQ2095; JQ2096.

PIR, JQ2096; JQ2096.

PIR, JQ2099; JQ2099.

PIR, JQ2099; JQ2099.

PIR, JQ2100; JQ2100.

PIR, JQ2101; JQ2101.

PIR, JQ2101; JQ2102.

PIR, JQ2102; JQ2102.

PIR, JQ2102; JQ2102.

PIR, JQ2103; JQ2103.

PIR, JQ211; JQ2112.

PIR, JQ2112; JQ2112.

PIR, JQ2114; JQ2111.

PIR, JQ2115; JQ2112.

PIR, JQ2116; JEA.

PROMIPER, PIRH10832; Hepvir_surfAg; 1.

PFam; PPO0695; VMSA; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB029951; BAB20334.1; -; Genomic_DNA.
PIR, JQ2102; JQ2102.
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                                                               Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
NCBI_TaxID=10407;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Small surface polypeptide.
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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135.00
100.00%
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                                       Small surface polyprotein.
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Q9DUK6;
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145 GlyAsnCys 147
                                                                                                                                NUCLEOTIDE SEQUENCE.
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 106, Appli
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mass, Clifford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
US-09-721-480-7
US-08-750-797A-1
US-08-972-929B-3
US-08-932-929B-3
US-08-932-929B-3
US-09-247-990-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-10
US-09-724-969-12
US-08-458-110-214
US-08-458-110-214
US-08-458-101-214
US-08-458-101-216
US-08-468-101-216
US-08-488-551A-106
US-08-485-551A-106
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COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 26 West 61 Street
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09719528A; Patent No. 6558675; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chong Jin
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       APPLICANT: Oon,
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-LOOPEXT=0-UNITS=blts -START=1 -END=-1 -MATRIX=D0 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 40, Appl
Patent No. 5196194
Patent No. 5436139
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Patent No. 5164485
Sequence 2, Appli
Sequence 2, Appli
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2480.270 Million cell updates/sec
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                                                                                                                                                                    December 27, 2005, 20:44:58 ; Search time 45.4 Seconds
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62. /cgn2_6/prodaca1/iaa/RECOMB.pep:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                       using frame_plus_n2p model
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00 2 US-10-209-264-3

06 1 US-08-378-011A-3

06 1 US-08-378-011A-1

77 6 5164485-2

13 2 US-09-719-528A-2

13 2 US-10-209-264-2

14 2 US-09-710-573A-4

15 2 US-09-471-573A-4

16 6 5136139-5

17 0 2 US-09-721-480-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           572060 seqs, 82675679 residues
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1278
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext ,
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Match Length DB
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
 Chong Jin
Gek Keow
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1230.00
98.68%
98.68%
96.24%
                                                                NUMBER OF SEQUENCES: 11
                                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Percent Similarity:
Best Local Similarity:
  APPLICANT:
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                                                                                                                                                                                                                        1 ATGGAGAACACAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTC
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                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TELEPHONE: (212) 708-1800
INFORMATION FOR ESO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
                                         TYPE: amino acid

STRANDENNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTCTTTGGGTATACATT 678
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                                                                                                                      3.74e-124
1230.00
98.68%
98.68%
                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                              Alignment Scores:
Pred. No.:
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US-10-209-264-3
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CCAAGGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAACATCAACCACCAGGACGGGCC 359
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                                                                                                       HUMAN HEPATITIS B VIRAL STRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

COMPUTER: IN INTERPRET: IN COMPA:

APPLICATION NUMBER: BCT/8C98/00046

FILING DATE: 19-JAN-1998

ATTORNEY/AGENT INFORMATION:

NAME: MARS: ADS. Clifford J.

REFERENCE/DOCKET NUMBER: 30.086

REF
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Conservative:
Mismatches:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
Zhao, Yi
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUM
USES THEREOF
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(202) 659-2930

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Sequence 1, Application US/08378011A
Patent No. 5693497
 TELEPHONE:
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US-08-378-011A-1
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374 FTrpGlyArgSerLeuTyrAsnIleLeuSerProPheLeuProLeuLeuProllePhePh 394
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                                                                                          AAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCACCTGGGCTTTCGCAAG 479
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274 rGlnGlyMetLeuProValCysProLeuLeuProGlyThrSerThrThrSerThrGlyPr 294
                                               OCYSLYSThrCysThrThrProAlaGlnGlyAsnSerThrPheProSerCysCysTh
                                                                                                             rlysProSerAspGlyAsnCysThrCysIleProlleProSerSerTrpAlaPheAlaAr
                                                                                                                                                         ATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT
                                                                                                                                                                                                                                          ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: FUJITA, Hiroyuki
APPLICANT: MANABE, Sadao
APPLICANT: MANABE, Sadao
APPLICANT: MANABE, Sadao
APPLICANT: OSAME, Juichiro
APPLICANT: YOSHIDA, Iwao
APPLICANT: TAKAKU, Keisuke
APPLICANT: TAKAKU, Keisuke
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STRY: N.W. Suite 1000 CITY: Washington STATE: D.C. COUNTRY: U.S.A.

ZID: 20006
COMPUTRY: U.S.A.
ZIP: BADDIE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTRY: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version S.O
SOFTWARE: ASCII, genereated using Word Perfect, version DOSTWARE: ASCII, genereated using Word Perfect, version S.O
CLASSIFICATION NUMBER: US/08/378,011A
FILING DATE: 25-CAN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/061,518
FILING DATE: 18-JUN-1986
PRIOR APPLICATION NUMBER: US 07/061,518
FILING DATE: 15-JUN-1987
PRIOR APPLICATION NUMBER: US 07/061,518
FILING DATE: 15-JUN-1987
PRIOR APPLICATION NUMBER: US 07/061,518
FILING DATE: 15-JUN-1987
PRIOR APPLICATION NUMBER: US 07/061,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36.281
REPERENCE/DOCKET NUMBER: 870602B
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/08378011A; Patent No. 2653497; GENERAL INFORMATION:
APPLICANT: TAKAMIZAWA, Akihisa
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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US-08-378-011A-3
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                                                                                                                                                                                                                                                                                                                                                             US-10-761-006A-1_COPY_155_835 (1-681) x US-08-378-011A-3 (1-226)
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Matches:
Conservative:
Mismatches:
Indels:
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TELEFAN: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 226 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: Amino acid
NULECULE TYPE: protein
US-08-378-011A-3
                                                                                                                                                                                                      1.18e-121
1206.00
96.92%
96.92%
94.37%
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Best Local Similarity:
Query Match:
DB:
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70

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299

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61 TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCAAT 119
                                                                                                                                                 90 ellellePheLeuPhelleLeuLeuLeuCysLeullePheLeuLeuValLeuLeuAspTy 110
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ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5164485-2
; Patent No. 5164485
; Patent No. 5164485
; PAPLICANT: FUJISAWA, YUKIO; ITOH, YASUAKI; NISHIMURA, OSAMU; FUJII, TOMOKO
; TITLE OF INVENTION: MODIFIED HEPATITUS B VIRUS SURFACE; ANTIGEN P31 AND PRODUCTION THEREOF; NUMBER OF SEQUENCES: 22; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/547,948
; FILING DATE: 03-011-1990
; PRICH APPLICATION NUMBER: 898,425
; APPLICATION NUMBER: 898,425
; RILING DATE: 20-AUG-1986
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Matches:
Conservative:
Mismatches:
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Gaps:
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Best Local Similarity:
Query Match:
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LENGTH: 277
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GENERAL INFORMATION:
APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: PUJITA, Hiroyuki
APPLICANT: WANABB, Sadao
APPLICANT: WANABB, Sadao
APPLICANT: VOSHIDA, Iwao
APPLICANT: NOSHIDA, Iwao
APPLICANT: TAKAKU, Keisuke
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,011A
CLASSIFTATION NUMBER: US/08/378,011A
FILING DATE: 18-JUN-1995
CLASSIFTATION NUMBER: JP 61-143412
PRIOR APPLICATION NUMBER: US 07/061,518
PRIOR APPLICATION NUMBER: US 07/061,518
PRIOR APPLICATION NUMBER: US 07/061,518
PRILNG DATE: 13-JUN-1992
ATTONNEY/AGENT INFORMATION:
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,231
REFERENCE/DOCKET NUMBER: 870602B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
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TELECOMMUNICATION
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Matches:
Conservative:
Mismatches:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRAGTH: 236 amino acids
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1206.00
96.92%
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TOPOLOGY: linear
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Best Local Similarity:
Query Match:
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Matches:
Conservative:
Mismatches:
Indels:
ATTORNEY/AGENT INPORMATION:
NAME: MABS, CLIffford J.
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTEREISTICS:
LENGTH: 843 amino acids
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SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                   111 BSerProThrSerCyBProProIleCyBProGlyTyrArgTrpMetCyBLeuArgArgPh
                                                                                                                                                                                                                92 PheLeuGlyGlyAlaProThrCys-ProGlyGlnAsnSerGlnSerProThrSerAsnHi
                                                                                                                                           TATCATATICCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTCTTCTGGACTA
                                                                                                                                                                                                 CCAAGGIATGITGCCCCGTTTGTCCTCTCCAGGAACATCAACCACCAGCACGGGGC
                                                                                                                                                                                                                                                       360 ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTAC
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                                                                                                                                                                                                                                                                                                                                                                        480 ATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuThrArg11eLeuThr11eProG1nSerLeuAspSerTrpTrpThrSerLeuAsn
                                                                                     Zhao, Yi
Zhao, Wei Ning
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10033

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09719528A; Patent No. 6558626; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Oon, Chong Jin
Lim, Gek Keow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-719-528A-2
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423 ACCTTCGGACGGAAACTGCACTTGTATTCCCATCCATCATCCTGGGCTTTCGCAAGATT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetGluAsnThrThrSerGlyPheLeuGlyProLeuLeuValLeuGlnAlaGlyPhePhe
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                                                                     AGGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAACATCAACCACCAGCACGGGGCCATG
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OTHER INFORMATION: Wild-type HBsAg amino acid sequece
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Matches:
Conservative:
Mismatches:
Indels:
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| Sequence 2, Application US/09471573A
| Patent NO. 6551820
| GENERAL INFORMATION:
| APPLICANT: Mason, Hugh
| APPLICANT: Thansvala, Yasmin
| TITLE OF INVENTION: Expression of Immunogenic
| TITLE OF INVENTION: Plants
| FILE REFERENCE: 3121/1080
| CURRENT FILING DATE: 1999-12-23
| PRIOR APPLICATION NUMBER: 60/113,827
| PRIOR APPLICATION NUMBER: 60/113,827
| PRIOR APPLICATION NUMBER: 60/113,827
| SOFTWARE: Patentin version 3.0
| SEQ ID NOS: 41
| SOFTWARE: Patentin version 3.0
| TOWNEY FOR THE PATENTIAL PAT
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Query Match:
DB:
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US-09-471-573A-2
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                                                                                                                                          Zhao, Yi
Zhao, Wei Ning
Chen, Wei Ning
TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/209,264
FILING DATE: 31-Jul-2002
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 708-1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 843 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
                                        Sequence 2, Application US/10209264
Patent No. 6787142
GENERAL INFORMATION:
                                                                                                             APPLICANT: Oon, Chong Jin
Lim, Gek Keow
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STATE: New York
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Best Local Similarity:
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                       -10-209-264-2
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DB:
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FPACENT NO. 2196194

FPACENT NO. 2196194

TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN NUMBER OF SEQUENCES: 21

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/679,621

FILING DATE: 7-DEC-1984

FRIOR APPLICATION DATA:

FILING DATE: 12-UUL-1983

APPLICATION NUMBER: 107,267

FILING DATE: 21-DEC-1979

FILING DATE: 21-DEC-1979

FILING DATE: 24-MAY-1979
                                      US-10-761-006A-1_COPY_155_835 (1-681) x US-09-471-573A-40 (1-226)
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US-09-471-573A-40

US-09-471-573A-40

Sequence 40, Application US/09471573A

Sequence 40, Application US/09471573A

Sequence 40, Application US/09471573A

GENERAL INFORMATION:
APPLICANT: Mason, Hugh

TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transge
TITLE OF INVENTION: Plants

TITLE OF INVENTION: Blants

TITLE OF INVENTION: Plants

TITLE OF INVENTION WINBER: 09/09/471,573A

CURRENT APPLICATION NUMBER: 06/113,827

PRIOR PILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENT VERSION 3.0
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                                                                                              TCAGTGGTTCGTAGGGCTTTCCCCCCACTGTTTGGCTTTCAGTTATAGGATGATGTGGTA
  LeuLeuThrArgIleLeuThrIleProGlnSerLeuAspSerTrpTrpThrSerLeuAsn
                                          240 TAICATATICCICITCAICCIGCIGCIAIGCCICAICTICITGITGTITCTICGACIA
                                                                                 CTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATCGCTGGATGTGTCTGCGGCGTTT
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-471-573A-40
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Pred. No.:
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LENGTH: 226
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Matches:
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FILING DATE: 21-DEC-1979

APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979

SEQ ID NO:5:
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                                                                                            OTHER INFORMATION: Description of Artificial Sequence: pCMVII opti
OTHER INFORMATION: 330 E1/SAg
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Matches:
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Indels:
TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE FILE REFERENCE: PP01655.002 CURRENT APPLICATION NUMBER: US/09/721,480 CURRENT FILING DATE: 2000-11-22 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 390
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                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Conservative:
Mismatches:
Indels:
                                                                 APPLICANT: Selby, Mark
APPLICANT: Selby, Mark
APPLICANT: Glazer, Edward
APPLICANT: Houghton, Michael
TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
FILE REFERENCE: PP01635.002
CURRENT APPLICATION NUMBER: US/09/721,480
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.0
US-09-721-480-7; Sequence 7, Application US/09721480; Patent No. 6740323; GENERAL INFORMATION:
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1163.00
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91.63%
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LENGTH: 531
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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359 425 419 445 479 465 485

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Patent No. 5928902
GENERAL INFORMATION:
GANERAL INFORMATION:
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HB8AG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
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STATE: ALLES OF STATE: PARA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/42,612
APPLICATION NUMBER: 08/42,612
APPLICATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
REFERENCE/POCKET NUMBER: B45015-1C2
TELEPHONE: 610-270-5096
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TTGGGGGCGAAGTCTGTACAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTT
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                                                                                                                                                                                                                                             US-08-760-797A-1

'Sequence 1, Application US/08760797A

'Sequence 1, Application US/08760797A

'Patent No. 5928902

'GENERAL INFORMATION:

APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph

'TILLE OF INVENTION: Hybrid Protein Between CS

'TILLE OF INVENTION: Hybrid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
OPERATIOS SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/442,612
APPLICATION NUMBER: 08/442,612
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
NAME: Baumeister, Kirk
NAME: Baumeister, Kirk
TELEFORMUTCATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELEFORMUTCATION INPORMATION:
TELEFORMUTCATION INPORMATION:
TELEFORMUTCATION INPORMATION:
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LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
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Matches:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-797A-3
                                                                                                              1.4e-116
1160.00
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TELEFAX: 610-270-5090
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OGULTA Y., KAROMANE.

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AB02963; BAB20346.1; -; Genomic_DNA.

PIR; JQ2094; JQ2094.

PIR; JQ2095; JQ2096.

R PIR; JQ2096; JQ2096.

R PIR; JQ2099; JQ2099.

R PIR; JQ2099; JQ2099.

R PIR; JQ2100; JQ2100.

R PIR; JQ2100; JQ2100.

R PIR; JQ2100; JQ2100.

R PIR; JQ2101; JQ2101.

R PIR; JQ2101; JQ2101.

R PIR; JQ2108; JQ2108.

R PIR; JQ2109; JQ2109.

R PIR; JQ2101; JQ2111.

R PIR; JQ2101; JQ2111.

R PIR; JQ2111; JQ2111.

R PIR; JQ2112; JQ2111.

R PIR; JQ2112; JQ2111.
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Orthohepadnavirus.
NCBI_TaxID=10407;
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Last annotation update)
0801M3_HPBV0
091GM7_HPBV0
090ZT1 HPBV0
09DUJ5_HPBV0
09DUJ5_HPBV0
09GZT1_HPBV0
09GZT1_HPBV0
09GZT1_HPBV0
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09DUG1_HPBV0
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PANTHER; PTHR10832; Hepvir surfAg; 1.
Pfam; PP00695; vMSA; 1.
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Q9DUJ4;
01-MAR-2001 (TrEMBLrel. 16, C.
01-MAR-2001 (TrEMBLrel. 16, L.
01-OCT-2003 (TrEMBLrel. 25, L.
Small surface polyprotein.
  Polyprotein.
226 AA; 2
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Q7tds6 hepatitis b
Q9dha2 hepatitis b
Q80gul3 hepatitis b
Q4fd2 hepatitis b
Q5sdk8 hepatitis b
Q5sdk8 hepatitis b
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Q9x14 hepatitis b
Q9x14 hepatitis b
Q6xp7 hepatitis b
Q7td7 hepatitis b
Q7td7 hepatitis b
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                      frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2166443 seqs, 705528306 residues
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Q8GGU3_HPBVO
Q8GGU5_HPBVO
Q5BGU5_HPBVO
Q51GW8_HPBVO
Q91GW8_HPBVO
Q99CZG_HPBVN
Q99W96G_HPBVN
Q9YKI9_HPBVN
Q9YKI9_HPBVN
Q6KP7_HPBVO
Q7TDR4_HPBVO
Q8OMQ7_HPBVO
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2: uniprot_trembl:*
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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SEQUENCE
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TUDS6 HPBV0

OTDS6.

OTDS6.

O1-OCT-2003 (TERMBLE1. 25, Created)

O1-OCT-2003 (TERMBLE1. 25, Last sequence update)

O1-OCT-2003 (TERMBLE1. 26, Last sequence update)

O1-OCT-2003 (TERMBLE1. 26, Last sequence update)

PreS1/preS2 surface protein.

PreS1/preS2 surface protein.

Hepatitis B virus.

Viruses, Retro-transcribing viruses; Hepadnaviridae; Orthohepadnavirus.

NCBI_TAXID=10407;
                                                                                                                                 x Q9DUJ4_HPBV0 (1-226)
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Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen
            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                   Gaps:
                                                                                                                                 US-10-761-006A-1_COPY_155_835 (1-681)
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Best Local Similarity:
Query Match:
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QDDHA2;

QDCHA2;

01-MAR-2001 (TrEMBLrel. 16, Created)

01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                        US-10-761-006A-1_COPY_155_835 (1-681) x Q7TDS6_HPBV0
                                                                                           400 AA; 43790 MW; 5D2FFC9D91CFE4D7
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ
EMBL; AY167091; AAO41300.1; -; Genomic DNA.
GO; GO:0016032; P:viral life cycle; IEA.
PANTHER; PTHR10832; Hepvir surfAg.
PANTHER; PTHR10832; Hepvir surfAg; 1.
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254 299 419

539 354

629

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T1GGGGGGGGAAGTCTGAGAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTT
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 ATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTAGTGCCATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLECTIDE SEQUENCE.
STRAIN=FW1021;
Lin X., Zheng D.L., Xu X.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY206392; AAP06646.1; -; Genomic_DNA.
GO, GO.0016032; P:Virtal life cycle; IEA.
InterPro; IFR000349; Hepvir surfAg.
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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OBOGU3;

O1-JUN-2003 (TrEMBLrel. 24, C;

O1-JUN-2003 (TrEMBLrel. 24, L;

O1-OCT-2003 (TrEMBLrel. 25, L;

S protein.

Hepatitis B virus.
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1210.00
97.36%
96.92%
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Best Local Similarity:
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                                                                                                            Coura Y., Kurosaki M., Asahina Y., Enomoto N., Marumo F., Sato C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL, AB0229946; BAB20369-1; -; Genomic_DNA.

R PIR, JQ2094; JQ2094.

R PIR, JQ2095; JQ2095.

R PIR, JQ2099; JQ2099.

R PIR, JQ2099; JQ2099.

R PIR, JQ2100; JQ2100.

R PIR, JQ2109; JQ2100.

R PIR, JQ2109; JQ2100.

R PIR, JQ2109; JQ2109.

R PIR, JQ2109; JQ2109.
                                                                                                                   .
:
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Small surface polyprotein.
Name-CG37; Synonyms=CG28;
Name-CG37; Synonyms=CG28;
Viruses; Betroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-761-006A-1\_COPY_155_835 (1-681) \times Q9DHA2\_HPBV0 (1-226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AA; 25406 MW; 25F97F2880749EEE CRC64;
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221
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR000349; Hepvir surfag.
PANTHER; PTHR10832; Hepvir surfag; 1.
Pfam; PF00695; vMSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.78e-99
1212.00
97.36%
97.36%
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PIR, JQ2112; JQ2112.
PIR, JQ2116.
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SEQUENCE 226 AA; 2
                                                                                                      NUCLEOTIDE SEQUENCE.
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BMBL; DQ089801; AAZ05311.1; -; Genomic DNA.

SEQUENCE 400 AA; 43707 NW; 2CDF00845325EFD8 CRC64;
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NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=10407;
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NUCLEOTIDE SEQUENCE.

STRAIN-FMUO11;
LIN X., Zheng D.L., Xu X.;
Lin X., Zheng D.L., Xu X.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ
EMBL, AY206392; AAP06644.1; -; Genomic_DNA.
GO, GO:0016032; P:viral life cycle; IEĀ.
INTERPE, PTRR10932; Hepvir_gurfAg.
PANTHER; PTRR10932; Hepvir_gurfAg.
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Q80GUS;
Q1-JUN-2003 (TrEMBLrel. 24, La
Q1-JUN-2003 (TrEMBLrel. 24, La
Q1-OCT-2003 (TrEMBLrel. 25, La
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Hepatitis B virus.
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01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
HBRAG.
HBRAG.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
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Matches:
Conservative:
Mismatches:
Indels:
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PANTHER; PTHR10832; Hepvir_surfAg;
Pfam; PR0685; WMSA; 1.
Antigen; Envelope protein.
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SONG B.-C., Kim H., Kim S.-H., Cha C.-Y., Kook Y.-H., Kim B.-J.,
"Comparison of full length sequences of hepatitis B virus isolates hepatocellular carcinoma patients and asymptomatic carriers of Norea.",
J. Med. 'Virol. 75:13-19(2005).
EMBL, AY61560; AAV52022.1; -; Genomic_DNA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0010031; D:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_BurfAg.
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334 gPheLeuTrpGluTrpAlaSerValArgPheSerTrpLeuSerLeuLeuValProPheVa 354
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MEDLINE=2028425; PubMed=11074476;
MEDLINE=2028425; PubMed=11074476;
DOI=10.1002/1096-9071(200012)62:4<471::AID-JMV12>3.3.CO;2-O;
Rokuhara A., Tanaka E., Yagi S., Mizokami M., Hashikura Y.,
Kawasaki S., Kiyosawa K.;
"De novo infection of hepatitis B virus in patients with orthotopic liver transplantation: analysis by determining complete sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA; 25394 MW; 835E71D8909A9C21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPX13;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Surface antigen.
Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                  226 AA
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J. Med. Virol. 62:471-478(2000).
EMBL; AB030517; BAA82654.1; -; Genomic_DNA.
EMBL; AB030516; BAA82653.1; -; Genomic_DNA.
PIR; JQ2094; JQ2094.
PIR; JQ2095; JQ2095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, JQ2112; JQ2112.

PIR, JQ2112; JQ2116.

POR, GO:016032; P:Viral life cycle; IEA.

InterPro; IRR000349; Hepvir_surfag.

PANTHER; PTHR10832; Hepvir_surfag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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1207.00
96.92%
96.92%
                                                                                                                                                                                                                                                                                                                                                QPPX13 HPBV0 PRELIMINARY;
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JQ2097; JQ2097.
JQ2098; JQ2098.
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702100) JQ2100.
702101) JQ2101.
702102, JQ2102.
702106, JQ2106.
702109, JQ2109.
702109, JQ2109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10407;
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SEQUENCE
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PIR;
PIR;
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Q9PX13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 LeuLeuThrArglleLeuThrIleProGlnSerLeuAspSerTrpTrpThrSerLeuAsn 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITICIAGGGGGGGCACCACGTGITCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 ATGCAAGACCTGCACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTTTGTTGCTGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 PheLeuGlyGlyAlaProThrCys-ProGlyGlnAsnSerGlnSerProThrSerAsnHi
                                                                                Shi S., Dong J., Huangfu J.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AX040799; AXX94658.1; -; Genomic_DNA.
PIR; JQ2095; JQ2095.
PIR; JQ2095; JQ2096.
PIR; JQ2099; JQ2096.
PIR; JQ2099; JQ2099.
PIR; JQ2099; JQ2099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-761-006A-1_COPY_155_835 (1-681) x Q91GW8_HPBV0 (1-400)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 AA; 43682 MW; 283E506EE6157CAF CRC64;
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1220
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Matches:
Conservative:
Mismatches:
Indels:
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PIR; JQ2095; JQ2095.

PIR; JQ2096; JQ2095.

PIR; JQ2099; JQ2099.

PIR; JQ2099; JQ2099.

PIR; JQ2010; JQ2100.

PIR; JQ2100; JQ2100.

PIR; JQ2101; JQ2101.

PIR; JQ2101; JQ2101.

PIR; JQ2101; JQ2101.

PIR; JQ2101; JQ2110.

PIR; JQ2111; JQ2110.

PIR; JQ2111; JQ2111.

PIR; JQ2112; JQ2112.

PIR; JQ2112; JQ2112.

PIR; JQ2112; JQ2112.

PIR; JQ2112; JQ2112.

PIR; JQ2112; JQ2114.

PIR; JQ2112; JQ2114.

PIR; JQ2114; JQ2114.

PIR; JQ2144; JQ2114.

PIR; JQ2144; JQ2144.

PIR; JQ2144; JQ2144.

PIR; JQ2144.

PI
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1208.00
97.36%
96.92%
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                                                              NUCLEOTIDE SEQUENCE
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Best Local Similarity:
Query Match:
Orthohepadnavirus
             NCBI TaxID=10407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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SEQUENCE
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266 rGlnGlyMetLeuProValCy8ProLeuLeuProGlyThrSerThrThrSerThrGlyPr 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 sSerProThrSerCysProProlleCysProGlyTyrArgTrpMetCysLeuArgArgPh
                                                                                                                                                                                                                                                                                                                                               167 MetGluAsnThrThrSerGlyPheLeuGlyProLeuLeuValLeuGlnAlaGlyPhePhe
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Mismatches:
Indels:
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                                                                                                                                                                                                         Length:
Matches:
PIR; JQ2106; JQ2106.
PIR; JQ2109; JQ2109.
PIR; JQ2109; JQ2109.
PIR; JQ2112; JQ2111.
PIR; JQ2112; JQ2111.
PIR; JQ2116; JQ2116.
GO; GO:0019031; C.viral envelope; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_surfAg.
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                                                                                                                                                  Antigen; Envelope protein.
SEQUENCE 392 AA; 42699 MW;
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1207.00
96.92$
96.92$
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Best Local Similarity:
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Pred. No.:
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rTrpGlyProSerLeuTyrAsnIleLeuSerProPheLeuProLeuLeuProIlePhePh
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A Zhong Y.W., Shi S.S., Yang J.Z., Liu Y.;
L Submitted (NOV.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF191303; AAF05722.2; -; Genomic_DNA.
R PIR; JQ2094; JQ2096.
R PIR; JQ2095; JQ2096.
R PIR; JQ2099; JQ2099.
R PIR; JQ2099; JQ2099.
R PIR; JQ2099; JQ2099.
R PIR; JQ2109; JQ2109.
R PIR; JQ2101; JQ2101.
                                                                                                                                                                                            TATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTCTTCTGGACTA
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     MetGluAsnThrThrSerGlyPheLeuGlyProLeuLeuValLeuGlnAlaGlyPhePhe
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                              TCGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTC-TGGTGGACTTCTCTCAAT
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Hepatitis B virus (subtype adr).
Viruses, Retro-transcribing viruses; Hepadnaviridae;
Octhohepadnavirus.
NCBI_TaxID=106820;
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O9CCZ6;
O9CCZ6;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NUCLEOTIDE SEQUENCE.
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MEDLINE=20528425; PubMed=11074476;
MEDLINE=20528425; PubMed=11074476;
DOI=10.1002/1096-9071 (20012)62:4<471::AID-JMV12>3.3.CO;2-O;
Rokuhara A., Tanaka E., Yagi S., Mizokami M., Hashikura Y.,
Kawasaki S., Kiyosawa K.;
"De novo infection of hepatitis B virus in patients with orthotopic liver transplantation: analysis by determining complete sequence of the genome.";
                                                                                                                        Synonyms=OG17, OG18, OG22, OG25, OG27, OG31, OG32, OG33, OG36, OG38,
OG39, OG40, OG42;
Hepatitis B virus.
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                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Main protein (Small surface polyprotein) (Surface antigen) (Small
                                                                                                                                                                                                                                                                                                                                       Ogura Y., Kurosaki M., Asahina Y., Enomoto N., Marumo F., Sato
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Sun X., Rokouhara A., Tanaka E., Gad A., Mutou H., Matsumoto
Yoshizawa K., Kiyosawa K.;
"Nucleotide Mutations Associated With Hepatitis B e Antigen
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"Establishment of the consensus sequence of hepatitis prevailing in the mainland of China.";
Chin. J. Microbiol. Immunol. 19:189-2000(1999).
                                                                                                                                                                Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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Submitted (JAN-2005) to the EMBL/GenBank/DDBJ dat

REMBL, Y18866; CABB3764.1; -; Genomic_DNA.

REMBL, AB029971; BAB20350.1; -; Genomic_DNA.

REMBL, AB029971; BAB20357.1; -; Genomic_DNA.

REMBL, AB029976; BAB20357.1; -; Genomic_DNA.

REMBL, AB029980; BAB20359.1; -; Genomic_DNA.

REMBL, AB029980; BAB20363.1; -; Genomic_DNA.

REMBL, AB029981; BAB20363.1; -; Genomic_DNA.

REMBL, AB029982; BAB20363.1; -; Genomic_DNA.

REMBL, AB029989; BAB20363.1; -; Genomic_DNA.

DR EMBL, AB029989; BAB20310.1; -; Genomic_DNA.

DR EMBL, AB029989; BAB20370.1; -; Genomic_DNA.

DR EMBL, AB029999; BAB20371.1; -; Genomic_DNA.

DR EMBL, AB029991; BAB20371.1; -; Genomic_DNA.

DR EMBL, AB039991; BAB20371.1; -; Genomic_DNA.
              226 AA
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              PRT;
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STRAIN=HBV-C5, and HBV-C4;
           Q9W966 HPBVO PRELIMINARY,
Q9W966;
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NUCLEOTIDE SEQUENCE.
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SEQUENCE 226 AA; 25418 MW; 2D5BEE91908A7E00 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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PIR; JQ2098; JQ2098.

PIR; JQ2009; JQ2099.

PIR; JQ2100; JQ2100.

PIR; JQ2101; JQ2101.

PIR; JQ2102; JQ2102.

PIR; JQ2108; JQ2108.

PIR; JQ2109; JQ2108.

PIR; JQ2111; JQ2111.

PIR; JQ2112; JQ2111.

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Suropean Bioinformatics Institute. There are no restrictions on its lass long as its content is in no way modified and this statement is not
                                                                                                                                            oCysLysThrCysThrIleProAlaGlnGlyThrSerMetPheProSerCysCysTh 140
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Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.;
Takeshima H., Inokoshi J., Namiki M., Shimada J., Omura S.;
Takeshima H., Irokoshi J., Namiki M., Shimada J., Omura S.;
"Structural analysis of the gene coding for hepatitis B virus surface antigen and its product.";
J. Gen. Virol. 66:195-200(1985).
-!- PTM: Myristyolation is essential for viral infectivity (By similarity).
                                                                  rGlnGlyMetLeuProValCy8ProLeuProGlyThrSerThrThrSerThrGlyPr
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CCAAGGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAACATCAACCACCAGCACGGGGCC
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Ono Y., Onda H., Sasada R., Igarashi K., Sugino Y., Nishioka K.;
The complete nucleotide sequences of the cloned hepatitis B virus
DNA; subtype adr and adw. ";
Nucleic Acids Res. 11:1747-1757 (1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis B virus (subtype adr).
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
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13-SEP-2005 (Rel. 48, Last annotation update)
Major surface antigen precursor.
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PANTHER; PTHR10832; Hepvir surfAg; 1.
Pfam; PF00695; vMSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            678
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE OF 175-349
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13-SEP-2005 (Rel. 48, Last seq
13-SEP-2005 (Rel. 48, Last ann
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                                                                                                                                                                                                                                                                                                           Guo Y., Hou J.;

"Establishment of the consensus sequence of hepatitis B virus prevailing in the mainland of China.";

Chin. J. Midroblol. Immunol. 19:189-2000(1999).

EMBL; Y18858; CAB38772.1; -; Genomic_DNA.

PIR; JQ2094; JQ2094.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA; 25452 MW; 9A368436FDE2D9C7 CRC64;
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220
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Orthohepadnavirus.
                                                                                                                 Created)
Last sequence update)
Last annotation update)
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Mismatches:
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Matches:
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GO, GO:0016032, P:viral life cycle; IEA.
InterPro; IPR000349; Hepvir suffAg.
PANTHER; PTHR10832; Hepvir SuffAg; 1.
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      1.63e-98
1206.00
96.92%
96.92%
94.37%
                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                   Q9YKI9_HPBV0 PRELIMINARY;
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JQ2096.
JQ2097.
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NUCLEOTIDE SEQUENCE.
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JO2112; JO2112
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Best Local Similarity:
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JQ2100;
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JQ2108;
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DB:
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                                                                                                 Liu C.-J., Chen D.-J., Chen D.-S., Kao J.-H., Lai M.-Y.;
"Origin of Serum Hepatitis B Virus in Acute Exacerbation: with HBV in the Liver and from other Exacerbation.";
Hepatology 40:310-317(2004).
EMBL, AY556108; AAU01945.1; -; Genomic DNA.
GO, GO:0016032; P:Viral life cycle; IEA.
InterPro: IPR000349; Hepvir surfAg:
PANTHER; PTHR10832; Hepvir surfAg: 1.
Antigen.
SEQUENCE 400 AA, 43768 MW; DBDC9D063A569678 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
PreSI/preS2 surface.
Hepatitis B virus.
Ortubese; Retro-transcribing viruses; Hepadnaviridae;
Orthobeadnavirus.
Orthobeadnavirus.
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Matches:
Conservative:
Mismatches:
Indels:
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                Major surface antigen.

N.myristoyl glycine (by host) (By similarity).

N.linked (GlCNAc. .) (Potential).

M. 3C7437A6EEDBD4E6 CRC64;
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DID QG8RP7-HPBVO PRELIMINARY;
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Percent Similarity:
Best Local Similarity:
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           540 TCAGTGGTTCGTAGGGCTTTCCCCCCACTGTTTGGCTTTCAGTTATATGGATGATGTA
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TITCTAGGGGGAGCACCCACGTGTTCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCA
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                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.

Liu C.-J., Chen P.-J., Lai M.-Y., Kao J.-H., Chen D.-S.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AXI67095; AAO41312.1; -; Genomic_DNA.

GO; GO:0016032; P:viral life cycle; IEA.

InterPro; IPR000349; Hepvir_surfAg.

PANTHER; PTHR10932; Hepvir_surfAg; 1.

PERM; PF00695; VMSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-761-006A-1_COPY_155_835 (1-681) x Q7TDR4_HPBV0 (1-400)
                                                                                                                                                                                                                                                                                                                                                         400 AA; 43694 MW; CCF173EA4365E414 CRC64;
                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PreS1/preS2 surface protein.
Hepatitis B virus.
Viruses; Retro-transcribing viruses; Hepadnaviridae;
Orthohepadnavirus.
NCBI_TAXID=10407;
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                                                                                                           O7TDR4_HPBV0 PRELIMINARY;
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Title: Perfect

Run on:

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large surface antigen - hepatitis B virus (subtype adr)

Ny Contains: major surface antigen, middle surface antigen

C; Species: hepatitis B virus, HBV

C; Species: hepatitis B virus, HBV

C; Date: 14-Nov-1983 #text_change 09-Jul-2004

C; Accession: A03705; S04569; JQ2107; PQ0608

R; And H, Sasada, R; Igarashi, K.; Sugino, Y.; Nishioka, K.

Nucleic Acids Res. 11, 1747-1757, 1983

A; Title: The complete nuclectide sequences of the cloned hepatitis B virus DNA; subtype A; Recence number: A93460; MUD: 83168919; PMID: 6300776

A; Rocession: A03705

A; Relevance Lype: DNA

A; Relevance: UNIPROT: P03140; UNIPARC: UPI00001389C1; GB: V00867

A; Rho, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S.

Nucleic Acids Res. 17, 2124, 1989

A; Title: The nuclectide sequence and reading frames of a mutant hepatitis B virus subty A; Reference number: S04569; MUD: 89183619; PMID: 2928116

A; Reference number: S04569

A; Status: translation not shown

A; Molecule type: DNA

A; Residues: 1-50, 78, 52-66, 79, 69-129, 70, 131-142, 79, 144-164, S', 166-176, S', 178-338, A; Cross references: UNIPARC: UPI000017496C; EMBL: X14193

B; Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius J. Gen. Virol: 74, 1341-1348, 1993

A; Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A; Reference number: JQ2044; MUD: 93323382; PMID: 8336122

A; Accession: S020044; MUD: 93323382; PMID: 8336122
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A; Realdues: 175-400 < NOR>
A; Realdues: 175-400 < NOR>
A; Cross-references: UNIPARC: UP10000033737
A; Experimental source: genogroup C, subtype adr, strain pBRHBadr4
B; Norder, H.; Courouce, A.M.; Magnius, L.O.
Gen. Virol. 73, 3141-3145, 1992
A; Title: Molecular basis of hepatitis B virus serotype variations within the four major A; Reference number: PQ0453; MUID: 93107848; PMID: 1469353
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A; Accession: PQ0608
                       Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=Cgn2_1VGFT0 5pool pVG10761006/runat_27122005_192901_15763/app_query.fasta_1.1102
-Q=Cgn2_1VGFT0 5pool pVG10761006/runat_27122005_192901_15763/app_query.fasta_1.1102
-DB=FIR -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOÖPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LILST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWT=pct -NORMeact + HEAPSIZE=500 -MINIRN=0 -MAXIEN=2000000000
-USRR=USI0761006_@CGN_1 1_77_@runat_27122005_192901_15763 -NCPU=6 -LCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                         using frame_plus_n2p model
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A,Molecule type: DNA
A,Residues: 275-354 <NO2>
A,Cross-references: UNIPARC:UP1000017496D
A,Experimental source: subtype adrq+, Bau
C,Genetics:
A,Gene: pre-S1/pre-S2/S
A,Gene: pre-S1/pre-S2/S
B,Genetics:
C,Superfamily: hepatitis B virus surface antigen
C,Reywords: glycoprotein; surface antigen
E,120-400/Product: middle surface antigen (gene pre-S2/S) #status predicted
F):175-400/Product: major surface antigen (gene S) #status predicted <8:175-400/Product: major surface antigen (gene S) #status predicted <8:15,123,117/Binding site: carbohydrate (Asn) (covalent) #status predicted
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JQ2112
surface antigen - hepatitis B virus (subtype adr, strain 1763/92)
                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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C;Species: hepatitis B virus, HBV
C;Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 31-Dec-2004
C;Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 31-Dec-2004
C;Accession: J02112
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: J02044; MUID:93329382; PMID:8336122
A;Contents: genogroup C
A;Accession: J02112
A;Molecule type: DNA
A;Residues: 1-226 cNOR>
A;Residues: 1-226 cNOR>
A;Residues: 1-226 cNOR>
A;Cross-references: UNIPROT:091703; UNIPROT:09DUK5; UNIPROT:099UK6; UNIPROT:09DUK5; UNIPROT:09DUK6; UNIPRO
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Surface antigen - hepatitis B virus (subtype adr, strain pNDR260)
C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: JQ2110
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius B;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origit A;Reference number: JQ2044; MUID:93329382; PMID:8336122
A;Contents: genogroup C
A;Accession: JQ2110
A;Accession: JQ2110
A;Accession: JQ2110
A;Residues: 1-226 cNOR>
A;Conserveferences: UNIPROT:Q9QMX3; UNIPARC:UPI000017841E
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Cispecies: hepatitis B virus, HBV
Cispecies: hepatitis B virus, HBV
Cispecies: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
Cispecies: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
Cispecies: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
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Conservative:
Mismatches:
Indels:
Gaps:
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1201.00
96.48%
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C,Keywords: surface antigen
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Best Local Similarity:
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A; Molecule type: DNA
A; Residues: 1-226 cNOR>
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A; Residues: 1-226 cNOR>
A; Residues: 1-226 cNOR>
A; Cross-references: UNIPROT:069599; UNIPARC:UPI00000F532E; GB:X75792; NID:9416082; PIDN
A; Cross-references: UNIPROT:0492 b. C.O.
J. Gen. Virol. 73, 3141-3145, 1992
A; Title: Molecular basis of hepatitis B virus serotype variations within the four major A; Reference number: PQ0453; MUID:93107848; PMID:1469353
A; Molecule type: DNA
A; Residues: 101-180 cNO2>
A; Residues: 101-180 cNO2>
A; Experimental source: subtype adrq+, Oll
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JQ1576
major surface antigen - hepatitis B virus (subtype adr, strain P8)
major surface antigen - hepatitis B virus (subtype adr, strain P8)
major surfaces hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
C;Datte: 31-Dec-1993 #sequence
C;Datte: 31-Dec-1993 #sequence
C;Accession: JQ1576; pg06065
B;Norder, H.; Hammas, B.; Loefdahl, S.; Courouce, A.M.; Magnius, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A;Title: Comparison of the amino acid sequences of nine different serotypes of A;Reference number: JQ1570; MUID:99268879; PMID:1588323
A;Accession: JQ1570.
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A;Gene:
A;Gene:
A;Gene:
A;Gene:
B;C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
C;Keywords: glycoprotein; surface (Asn) (covalent) #status predicted
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JQ2108

surface antigen - hepatitis B virus (subtype adr, strain 747/92)

C;Species: hepatitis B virus, HBV

C;Species: hepatitis B virus, HBV

C;Date: 03-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 31-Dec-2004

C;Accession: 032108

R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993

A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: 042044; MUID:93329382; PMID:8336122

A;Contents: genogroup C

A;Accession: JQ2108

A;Accession: JQ2108

A;Accession: JQ2108

A;Contents: J-226 <ANR>
A;Accession: JQ2108

A;Contents: UNIPROT:091743; UNIPROT:091557; UNIPROT:Q9BUKS; UNIPROT:Q9BUKS; UNIPROT:Q9BUS5; UN
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Matches:
Conservative:
Mismatches:
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Pred. No.:
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Gurface antigen - hepatitis B virus (subtype adr, strain pHBV1-1)
C.Species: hepatitis B virus, HBV
C.Species: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C.Accession: JQ2104
R.Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius A.Gen. Virol. "4, 1341-1349, 1993
A.Fitle: Genetic relatedness of hepatitis B viral strains of diverse geographical original A.Reference number: JQ2044; MUID:93329382; PMID:8336122
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A; Accession: UQ104
A; Accession: UQ104
A; Accession: UQ2104
A; Residues: 1-226 < NOR>
A; Residues: 1-226 < NOR>
A; Cross-references: UNIPROT: Q81100; UNIPROT: Q9J0VB; UNIPROT: Q81181; UNIPARC: UPI00000F3B
C; Genetics:
A; Gene: S
C; Superfamily: hepatitis B virus surface antigen
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C;Species: hepatitis B virus, HBV
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: PL0053 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: PL0053 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: PL0053 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
R;Okamoto, H:, Oui, S:, Wang, Y:; Itoh, Y:; Tsuda, F:; Tanaka, T:; Akahane, Y:; Miyakawa Mol. Immunol. 26, 197-205, 1989
A;Title: The loss of subtypic determinants in alleles, d/y or w/r, on hepatitis B surface A;Accession: PL0053; MUD:89143494; PMID:2465492
A;Accession: PL0053
A;Molecule type: DNA
A;Residues: 1-226 <OKA>
A;Residues: 1-226 <OKA>
A;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
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Surface antigen - hepatitis B virus (subtype adr, strain Bau)
c;Species: hepatitis B virus, HBV
c;Accession: J02098
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius J. Gen. Total: J4, 1341-1348, 1993
J. Gen. Mill: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: J02044; MUID:93329382; PMID:8336122
A;Accession: J02098
A;Molecule type: DNA
A;Residues: 1-226 <NORA
A;Residues: 1-226 <NORA
A;Residues: 100208
A;Molecule type: DNA
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US-10-761-006A-1_COPY_155_835 (1-681) x JQ2111 (1-226)
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Surface antigen - hepatitis B virus (subtype adr, strain Bes)

Species: hepatitis B virus, HBV

C;Species: hepatitis B virus, HBV

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004

C;Accession: JQ2111

R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993

A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: JQ2044; MUID:93329382; PMID:8336122

A;Contents: genogroup C

A;Accession: JQ2111

A;Molecule type: DNA

A;Residues: 1-226 <NORA

A;Residues: 1-226 <NORA

A;Cross-references: UNIPROT:091546; UNIPROT:099BURS; UNIPROT:099DUKS; UNIPROT:099DUKS; UNIPROT:099DUKS; UNIPROT:099DUKS; UNIPROT:091793; UNIPROT:099DUKS; UNIPROT:
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RESULT 12
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BUTTAL ADDATITIS B VITUS (SUDTYPE AGW, STRAIN DIWK146)
C;Species: hepatitis B Vitus, HBV
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: JO2115
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius J. Gen. Virol. 74, 1341-1348, 1993
J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Contents: genogroup C
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Indels:
            surface antigen
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           C;Superfamily: hepatitis B virus C;Keywords: surface antigen
                                                  2.28e-99
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A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_chang C;Accession: JC1002
R;Qi, Z.H.; Yan, J.; Xiong, W.J.; Cai, L.W.
Chinese Biochem. J. 4, 201-209, 1988
A;Title: Determination of the nucleotide sequence and studies A;Reference number: JC1002
A;Accession: JC1002
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A;Residues: 1-226 <QIZ>
A;Cross-references: UNIPROT:P30019; UNIPARC:UPI00001389BB
C;Genetics:
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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A; Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A; Reference number: JQ2044; MUID:93329382; PMID:8336122
A; Reference number: JQ2044; MUID:9329382; PMID:8336122
A; Accession: JQ2094
A; Molecule type: DNA
A; Mesidues: 1-226 <NOR;
A; Residues: 1-226 <NOR;
A; Residues: 1-226 <NOR;
A; Cross-references: UNIPROT:09EK9; UNIPROT:09DHS0; UNIPROT:09BUK5; UNIPROT:09EK9; UNIPROT:09PXA0; UNIPROT:0PXA0; UNIPRO
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Matches:
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      1341-1348, 1993
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C;Keywords: surface antigen
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C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Species: 0.3-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: 0.702094; PQ0604
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius,
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A;Accession: JQ2115
A;Molecule type: DNA
A;Residues: 1-226 <NOR>
A;Cross-references: UNIPROT:Q9QMI4; UNIPARC:UPI0000178437
C;Genetics:
A;Gene: S
C;Keywords: surface antigen
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large surface antigen - hepatitis B virus (isolate 09D09HCC)
NyAlternate names: envelope protein
NyAlternate names: envelope protein
CyContains: major surface antigen; middle surface antigen
CySpecies: hepatitis B virus, HBV
A,Variety: isolate 09D09HCC
CyAccession: T13469
Beequence_revision 13-Aug-1999 #text_change 09-Jul-2004
CyAccession: T13469
Arch. Virol. 143, 2313-2326, 1998
Arch. Virol. 143, 2313-2326, 1998
AyTitle: Hepatitis B virus genomic sequence in the circulation of hepatocellular carcin A;Reference number: Z17684; MUID:99129050; PMID:9930189
A;Accession: T13469
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                       CCCATCCCATCATCCTGGGCTTTCGCAAG
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A;Molecule type: DNA
A;Residues: 1-384 <TAK>
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C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
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C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Species: hepatitis B virus, HBV
C;Species: J3-6-1994 Hesquence_revision 03-Feb-1994 #text_change 31-Dec-2004
C;Accession: J02101; P00609
R;Norder, H.; Hammas, B.; Lee, S.D.; Bile, K.; Courouce, A.M.; Mushahwar, I.K.; Magnius, J. Gen. Virol. 74, 1341-1348, 1993
A;Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin A;Reference number: J02044; MUID:93329382; PMID:8336122
A;Contents: genegroup C
A;Reference number: J02044; MUID:93329382; PMID:8336122
A;Contents: genegroup C
A;Residues: 1-226 <NOR>
A;Residues: 1-226 <NOR
A;Residues: 1-220 <NOR
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A;Molecule type: DNA
A;Residues: 101-180 <NO2>
A;Cross-references: UNIPARC:UP10000178445
C;Genetics:
A;Gene: S
C;Keywords: surface antigen
                                                               TTGTCTTTGGGTATACATT 678
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Search completed: December 27, 2005, 21:01:53 Job time : 42.59 secs

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'note= " these residues are specifically claimed in claim
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/note= " these residues are specifically claimed in claim
23."
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large surface antigen; core protein; transactivating X protein;
hepatitis vaccine; HBV infection; hepatocellular carcinoma.
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Abb05219 I
Aau97646 I
Adw68808 I
Adw68808 I
Adw68824 I
Adw68824 Adwar11496 I
Aar11496 I
Aar11495 I
                         Adw68794 Adw688793 Adw688793 Adw688821 Adw68821 Aaw68825 Adw68815 Adw68815 Adw68819 
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Aae04711
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Aab80956
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AAR11409
ADW68794
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ADW68826
ADW68825
AAW65505
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AAR55288
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ADU69200
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ADY62464
AEA08824
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  Misc-difference 174.
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  RESULT 1
  -MODEL-frame+ n2p.model -DEV-xlp
-MODEL-frame+ n2p.model -DEV-xlp
-MODEL-frame+ n2p.model -DEV-xlp
-MODEL-frame+ n2p.model -DFV50061006/runat 27122005 192900 15743/app_query.fasta_1.1102
-Q=/cgn2_1/USFPTO spool p/US10761006/runat 27122005 192900 15743/app_query.fasta_1.1102
-DBCALIGA-200 -THR SCARE-pCT -THR MARS-100 -TRANS=human40.cdi -LIST-45
-DGCALIGN-200 -THR SCARE-pCT -THR MARS-100 -TAIGN-15 -MODE-LOCAL
-OGTEMT-pCC -NORM-ext -HEAPSIZE=500 -MINIMEN -0 -MAXIEN=200000000
-USRR-US10761006 @CGN_1_1476 @runat_27122005_192900_15743 -NCPU=6 -ICPU=3
-NO WMAP -LARGEUERY -NGG SCORES=0 -MINIMEN -DAPAICACA-100 -LONGING
-DBV INREOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOF=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
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Aae17024 Hepatitis
Aae17025 Hepatitis
Aar50965 Peptide c
Aar50968 Peptide c
Aar50968 Peptide c
Aar94433 HBV surfa
Aay94437 HB8Ag pep
Aae25520 Hepatitis
                                                                                                          (without alignments)
3320.243 Million cell updates/sec
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                                                                                             December 27, 2005, 20:40:32 ; Search time 18.262 Seconds
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139
1 ACGACTCCTGCTCAAGGAAA\...............AACCTTCGGACGGAAACTGC
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                 using frame plus n2p model
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22-JUN-2000; 2000GB-00015308. 06-OCT-2000; 2000GB-00024544.

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The present sequence is encoded by the genome of an isolated strain of Hepatitis B virus designated human Hepatitis B virus (HBV) surface antigen-'S-133 Oon strain (Met to Thr). The viral genome is deposited as ECCC accession numbers P97121501. P97121502 and P97121503. The nucleotide sequence was isolated from hepatocellular carcinoma (HCC). The nucleotide sequence encodes four overlapping proteins, which are a DNA polymerase, a large surface antigen, a core protein, and a transactivating X protein.

The large surface antigen differs from the wild type sequence in that it contains a Thr at position 133 of the wild type sequence instead of a Met. The proteins are used to produce antibodies. The proteins, contains antibodies can be used for detecting the novel HBV strain, The HBV polypeptides can also be used in hepatitis vaccines. The HBV novel strain polypeptides can be used to identify compounds for treating or preventing HBV infection or hepatocellular carcinoma
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                                                                                                                                                                                                                        New isolated hepatitis B virus strain, useful for, e.g. treatment of hepatitis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-761-006A-1_COPY_527_595 (1-69) x AAY54045 (1-400)
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(GOVE-) GOVERNMENT REPUBLIC SINGAPORE.
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                                                                Zhao Y,
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319 GlyAenCye 321
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                                                                                                                             WPI; 2000-106104/09.
N-PSDB; AAZ37088.
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Best Local Similarity:
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                                                                   Lim GK,
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                                                                Oon CJ,
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DB:
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ઠે g 8 셤 22-JUN-2001; 2001WO-GB002817.

WO200198333-A2

27-DEC-2001

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The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBCAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBCAg. The deleted region may be replaced by an epitope from a protein other than HBCAG, in which case the HBCAg acts as a carrier to present the epitope to the immune system. This chimeric protein or its conclete acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBC The nucleic acid encoding the protein may be used in gene therapy or also be used as the basis of a prophylactic vaccine acid may calso be used as the basis of a prophylactic vaccine against a range of disease, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabies, acquired communication proteory syndrome (AIDE), dengue fever, yellow fever, malaria, tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning, virus (HBV) adw subtype S antigen
                                                                                                                                                                                           New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis B virus; HBV; core antigen; HBCAg; immune system; typhoid; prophylactic; gene therapy; vaccine; hepatitis A virus; HAV; herpes; hepatitis C virus; HCV; influenza; foot-and-mouth disease; diarrhoea; tuberculosis; pollo; zables; acquired immunodeficiency syndrome; AIDS; dengue fever; yellow fever; malaria; whooping cough; salmonellosis; food poisoning; meningitis; gonorrhea; antiviral; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Matches:
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                                                                      (CELL-) CELLTECH PHARM LTD
                                                                                                        Li J, Pumpens P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38 AA;
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The peptide shows cross reactivity with anti-hepatitis B surface antigen (HBsAG) antiserum. The peptide comprises the "a" epitope of HBsAG, a group specific determinant of HBsAG. It can be used for the diagnosis of hepatitis B virus infection and in vaccines against the virus, particularly in combination with alum as adjuvant and with a myristic acid residue added to the amino terminus of the peptide. This sequence is an analogue of the sequence described in AARSO961. See also in AARSO962-70. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ThrThrProAlaGlnGlyAsnSerWetPheProSerCysCysCysThrLysProThrAsp 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis B virus; HBV; epitope; antigen; HBsAg; diagnosis; detection; vaccine; treatment; antiserum; adw; surface antigen; viral infection.
Hepatitis B virus; HBV; epitope; antigen; HBsAg; diagnosis; detection; vaccine; treatment; antiserum; adw; surface antigen; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) for use in diagnosis or vaccines for hepatitis B virus -
comprising oligomers of an epitope sequence of hepatitis B surface
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                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       (UNNA-) UNITED NATIONS IND DEV ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR50961 standard; peptide; 24 AA.
                                                                                                                                         /label= Other.
/note= "Met(0)."
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Best Local Similarity:
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                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                        30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                 01-SEP-1992;
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14-OCT-1994
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                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to modified proteins comprising hepatitis B virus (HBV) core antigen (HBcAg) wherein one or more of the four arginine repeats has been deleted and the protein comprising the C-terminal cysteine of HBcAg. The deleted region may be replaced by an epitope from a protein other than HBcAg, in which case the HBcAg acts as a carrier to present the epitope to the immune system. This chimeric protein or its nucleic acid is useful as a vaccine or in a method of prophylactic or therapeutic vaccination of the human or animal body, particularly against HBV. The nucleic acid encoding the protein may be used in gene therapy or DNA vaccination protocols. The chimeric protein or its nucleic acid may also be used as the basis of a prophylactic vaccine against a range of diseases, e.g. HBV, hepatitis A virus (HAV), hepatitis C virus (HCV), influenza, foot-and-mouth disease, polio, herpes, rabies, acquired immunodeficiency syndrome (AIDS), denaque fever, yellow fever, malaria, tuberculosis, whooping cough, salmonellosis, typhoid, food poisoning, diarrhoea, meningitis or gonorrhea. The present sequence is Hepatitis B virus (HBV) adw subtype S antigen
                                                                                                                                                                                                                                                                                                                                                                       New proteins comprising a modified hepatitis B core antigen, useful as a vaccine in prophylactic or therapeutic vaccination of the human or animal body, particularly against hepatitis B virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
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Conservative:
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                                                                                                                       22-JUN-2001; 2001WO-GB002817.
                                                                                                                                                              22-JUN-2000; 2000GB-0001530B.
06-OCT-2000; 2000GB-00024544.
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                                                                                                                                                                                                                                                                                                           WPI; 2002-098223/13.
N-PSDB; AAD27426.
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Best Local Similarity:
Hepatitis B virus
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                                        40200198333-A2
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14-OCT-1994
                                                                                 27-DEC-2001
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Peptide cross reactive with anti-HBsAg antiserum.

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Length: Matches: Conservative: Mismatches:

Indel8:

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The peptide shows cross reactivity with anti-hepatitis B surface antigen (HBsAG) antiserum. The peptide comprises the "a" epitope of HBsAg, a group specific determinant of HBsAg. It can be used for the diagnosis of hepatitis B virus infection and in vaccines against the virus, particularly in combination with alum as adjuvant and with a myristic an analogue of the sequence described in AARSO961. See also in AARSO962-70. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for use in diagnosis or vaccines for hepatitis B virus \cdot oligomers of an epitope sequence of hepatitis B surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular presentation, FHV; virion-like particle, capsid protein, capsomer, RNA-2 gene, epitope, HBV; vaccine.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                   (UNNA-) UNITED NATIONS IND DEV ORG.
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                                                                                                                                                                                                                                  Claim 2; Page 14; 26pp; English.
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(first entry)
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                                                                                                                  Rao KV,
                                                                                                                                            WPI; 1994-101123/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 AA;
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                           30-AUG-1993;
                                                        01-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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31-MAY-1996
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17-MAR-1994
                                                                                                                                                                          Peptide(s) 1
comprising o
                                                                                                                  Manivel V,
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                                                                                                                                                                                                         antigen.
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DB:
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                                                                                                                                                                                                                                                                                                                   The peptide shows cross reactivity with anti-hepatitis B surface antigen (HBsAG) antiserum. The peptide comprises the "a" epitope of HBsAG, a group specific determinant of HBsAG. It can be used for the diagnosis of hepatitis B virus infection and in vaccines against the virus, particularly in combination with alum as adjuvant and with a myristic acid residue added to the amino terminus of the peptide. Analogues of this sequence are described in AAR50962-70. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus; HBV; epitope; antigen; HBSAg; diagnosis; detection; vaccine; treatment; antiserum; adw; surface antigen; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide(8) for use in diagnosis or vaccines for hepatitis B virus comprising oligomers of an epitope sequence of hepatitis B surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide cross reactive with anti-HBsAg antiserum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                               (UNNA-) UNITED NATIONS IND DEV ORG.
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                                                                                                                                                                                                                                                                                         Claim 2; Page 14; 26pp; English
                                                                                                                                                                            SK;
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/label= MeLys
                                                                                                                  92AT-00001746
                                                                                     93WO-EP002342
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95.65%
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                                                                                                                                                                            Manivel V, Rao KV,
                                                                                                                                                                                                         WPI; 1994-101123/12
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Best Local Similari
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Modified-site
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                                                                                                                   01-SEP-1992;
                            WO9405698-A1
                                                                                     30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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14-OCT-1994
                                                         17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Synthetic.
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                                                                                                                                                                                                                                                                  antigen.
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AAR50968 RESULT

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22
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                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                  AAE2552
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                                                                                                                                                                                                                                                                                                           1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
                                                                                                                                                                                                                                                                                                                     2 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 21
                                                                                                                                                     ď
                                                                                        The B-cell epitope (AAR94433) of the hepatitis B virus surface protein may be inserted into the outward-directed [1, 12, 13, 12 or 13 loop of the Flock House virus capaid protein (AR88755). The capsid protein provides a conformationally suitable location for this (or other, see AAR94430-32 and AAR94434-45) heterologous peptides. A molecular presentation system is obtd. The FHV recombinant capsomer can be expressed in B. coli. Alternatively, expression in insect cells using a baculovirus vector results in prodn. of mature virus-like particles. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macroglobulin; immunogenic complex; hepatitis; surface antigen; HBsAg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immune response modulator alpha-2 macroglobulin complex useful in the treatment of HIV or hepatitis:
                                   molecular presentation system - comprising a viral protein from a ll insect virus in which heterologous amino acid sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBsAg peptide 124-147 for use in immunogenic complex.
                                                                                                                                                                                                                      777100
                                                                                                                                                                                                                                                                                       US-10-761-006A-1_COPY_527_595 (1-69) x AAR94433 (1-24)
                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                           Indels:
Tisminetzky S;
                                                                                                                                                                                                                                                                                                                                                                                                        AAY04027 standard; peptide; 24 AA.
                                                                         Disclosure; Page 7; 39pp; English.
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99US-00282826
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130.00
95.65%
91.30%
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(first entry)
Scodeller E,
                                                                                                                                                                                                                                                                                                                                                GGAAACTGC 69
                                                                                                                                                                                                                                                                                                                                                                  GlyAsnCys 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-601324/51.
                 WPI; 1996-139691/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pizzo SV, Gron H;
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                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; vaccine
                                                                                                                                                                                          24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - MO9950303-A2
                                                                                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1998;
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20-DEC-1999
Baralle FE,
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                                                                                                                                                                                                                                                                                                                                                61
                                                     inserted
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A beautic complex compliation (alpha-2M) having an inteact bain cuttured an analysis of a lapha-2-macroglobulin (alpha-2M) having an inteact bait region is claimed, in which the biomolecule is covalently bound to an amino acid residue of a clawed thiol ester of the alpha-2M, the amino acid residue being a glutamyl residue and/or a cysteinyl residue. Preparation of the complex comprises activation of alpha-2M with a nucleophilic compound followed by incubation with the biomolecule at elevated temperature. Covalent compound to from inteact biomolecule is the effect without use of a protease. The obtained complex may be used as an antigen for stimulating fimune response, e.g. in the form of a vaccine. Enhanced presentation of the biomolecule is provided, especially for those antigens which are poorly immunogenic. Reduction of immunodominance of particular epitopes is also provided. Preferably the biomolecule is an HIV antigen or a hepatitis virus antigen, or a peptide, fragment, hybrid or chimeric bepatitis virus antigen, or a peptide, fragment, hybrid or chimeric compatitis peptide which may be used in the complex. It represents the pattitis peptide which may be used in the complex. It represents the confidence of the confidence of the pattitis peptide which may be used in the complex. It represents the confidence of the process of the pattitis beyond the standardise OS field)
                                                              A stable complex comprising at least one intact biomolecule and activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response; macrophage; tumour; human immunodeficiency virus; HIV; cytostatic; antimicrobial; alpha2M; anti-HIV; virucide; HBsAg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-761-006A-1_COPY_527_595 (1-69) x AAY04027 (1-24)
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Mismatches:
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Matches:
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Claim 3; Page 77; 103pp; English
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(first entry)
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Best Local Similarity:
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04-NOV-2002
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Particles comprising chimeric hepadnavirus core antigen protein - contg. foreign aminoacid sequence comprising epitope of e.g. hepatitis A or B and human immuno-deficiency virus, used as vaccine.

WPI; 1991-103861/15. N-PSDB; AAQ11233.

Example 3, Page 10; 24pp; English

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The information retained to a stable complete Complete Complete with a nucleophilic group which is covalently bound to activated alpha-2-macroglobulin (alpha2M) with an intact bait region. The stable complete is useful for enhancing host immunocompetence and for preparing vaccines for preventing and treating disease states. It is useful for increasing immune response to a particular antigen, and for suppressing immune response to a particular antigen. It is most preferably useful for administering antigens recognised by the macrophage in view of the existence on the macrophage of receptors for alpha2M. It is useful for treating cancer or infection, where the isolated protein is derived from tumour, abnormal cells or infectious organism, and this protein can be used as an antigen and prepared in alpha2M complex which statement in need of such treatment. It can also be used for inducing immune response against human immunodeficiency virus (HTV) antigens, and chequities virus antigens. The present sequence is Hepsatities b virus curface antigen (HBBAA) peptide used in the exemplification of the unvention. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 21
Immune response modulator alpha-2 macroglobulin complex useful in the treatment of HIV or hepatitis.
                                                                               comprising an intact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis B surface antigen pPD1-110-148 complex epitope.
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Conservative:
Mismatches:
Indels:
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                                                                              invention relates to a stable complex
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                               Claim 3; Col 35; 34pp; English.
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90GB-00017728
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95.65%
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Best Local Similari
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13-AUG-1990;
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The insert encoding this epitope was ligated into the NheI restriction site of plasmid pPV-Nhe to recreate the NheI sites which code for Ala-Ser residues flanking the epitope. The recombinant plasmid was transformed into E.coli strain XL-I Blue. Positive clones were cultured to high density in nutrient broth and induced to express chimaeric protein comprising the desired epitope by addition of IPTG. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                             New oligo- or poly-peptide variants of hepatitis B surface antigen, useful for diagnosis of, and vaccination against, hepatitis infection, derived from strain HDB05, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; HBsAg; hepatitis marker; virucide; hepatotropic; antiinflammatory; DNA detection; vaccine; diagnostic; hepatitis B virus infection; selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus HBsAg surface antigen fragment #7.
                                                                                                                                                                                                                                                 0 0 1 1 1 1 3 4 3
                                                                                                                                                                                                                                                                                                                                     US-10-761-006A-1_COPY_527_595 (1-69) x AAR11409 (1-43)
                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                 Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADW68797 standard; protein; 51 AA.
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N-PSDB; ADW68786.
                                                                                                                                                                                                                                                                                                                                                                                                              GGAAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis B virus.
                                                                                                                                                                                                                                                                                       Similarity:
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                                                                                                                                                                                                            Sequence 43 AA;
                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarit
                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                 Query Match:
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Claim 3; SEQ ID NO 15; 61pp; German.

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This sequence represents novel oligo- and poly-peptides that are variants of the hepatitis B surface antigen (HBsAg). HBV strain HBDD5 was isolated from a patient with inflammation of the liver but an atypical reaction pattern of hepatitis markers. PCR amplification and sequencing indicated the 5 specified mutations in the 8 gene, relative to adw wild-type. These comparations and laused amino acid variations: 4 in the a-determinant region and the other close to it at residue 181. The products of the invention are used to detect specific antibodies of the products of primers for detecting hepatitis B virus (HBV) nucleic acid, as immunogens and antibodies (Ab) raised against HBSAg are used for detecting HBSAg including use in vaccination, diagnosis and screening of donated blood. The antibodies do not bind, or bind much less strongly, to the HBSAg from virus of genotype A, subtype adw. This sequence represents a fragment of HEPATITUS B virus (HBSAG) corresponding to residues 115-
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Sequence 51 AA;

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1121
                                                            US-10-761-006A-1_COPY_527_595 (1-69) x ADW68797 (1-51)
       Length:
Matches:
Conservative:
Mismatches:
                                      Indels:
                                            Gaps:
     1.23e-10
130.00
95.65%
91.30%
                                                                                                        69
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                     Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                                                                        61
                                     Query Match:
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11 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 30 RESULT 12 ADW68794

Hepatitis B virus HBsAg surface antigen fragment #4. ADW68794 standard; protein; 55 AA. 24-MAR-2005 (first entry) ADW68794; 

antigen; HBsAg; hepatitis marker; virucide; hepatotropic; antiinflammatory; DNA detection; vaccine; diagnostic; hepatitis B virus infection; selectable marker.

Hepatitis B virus.

WO2004113369-A1.

29-DEC-2004

17-JUN-2004; 2004WO-EP006515

(DADE-) DADE BEHRING MARBURG GMBH

20-JUN-2003; 2003DE-01028080

Krupka U;

WPI; 2005-066451/07. N-PSDB; ADW68783.

New oligo- or poly-peptide variants of hepatitis B surface antigen, useful for diagnosis of, and vaccination against, hepatitis infection, derived from strain HDB05, also related nucleic acid and antibodies.

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This sequence represents novel oligo- and poly-peptides that are variants of the hepatitis B surface antigen (HBBAG). HBV strain HBDO5 was isolated from a patient with inflammation of the liver but an atypical reaction pattern of hepatitis markers. PCR amplification and sequencing indicated the 5 specified mutations in the 8 gene, relative to adw wild-type. These mutations all caused amino acid variations: 4 in the a-determinant region of the other close to it at residue 181. The products of the invention have virucide, hepatotropic and antilnifiammatory activity. The products of the invention are used to detect specific antibodies, as immunogens and antibodies (Ab) raised against HBBAG are used for detecting HBBAG. Including use in vaccination, diagnosis and screening of donated blood. The antibodies do not bind, or bind much less strongly, to the HBBAG from virus of genotype A, subtype adw. This sequence represents a fragment of HBBAGITUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligo- or poly-peptide variants of hepatitis B surface antigen, useful for diagnosis of, and vaccination against, hepatitis infection, derived from strain HDB05, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen; HBsAg; hepatitis marker; virucide; hepatotropic; antiinflammatory; DNA detection; vaccine; diagnostic; hepatitis B virus infection; selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus HBsAg surface antigen fragment #3.
                                                                                                                                                                                                                                                                                                                                                US-10-761-006A-1_COPY_527_595 (1-69) x ADW68794 (1-55)
                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGACTCCTGCTCAAGGAAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADW68793 standard; protein; 60
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130.00
95.65%
91.30%
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N-PSDB; ADW68782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004113369-A1.
                                                                                                                                                                                                                                                                                                   Sequence 55 AA;
                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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RESULT 15
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                                   This sequence represents novel oligo- and poly-peptides that are variants of the hepatitis B surface antigen (HBsAg). HBV strain HBD05 was isolated from a patient with inflammation of the liver but an atypical reaction pattern of hepatitis markers. PCR amplification and sequencing indicated the S specified mutations in the S gene, relative to adw wild-type. These mutations all caused amino acid variations: 4 in the a-determinant region and the other close to it at residue 181. The products of the invention have virucide, hepatotropic and antiinflammatory activity. The products of the invention are used to detect specific antibodies, as probes or primers for detecting hepatitis B virus (HBV) nucleic acid, as immunogens and antibodies (Ab) raised against HBsAg are used for detecting HBsAg including use in vaccination, diagnosis and screening of donated blood. The antibodies do not bind, or bind much less strongly, to the HBsAg from virus of genotype A, subtype adw. This sequence represents a fragment of Hepatitus B virus surface protein (HBsAg) corresponding to residues 111-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New oligo- or poly-peptide variants of hepatitis B surface antigen, useful for diagnosis of, and vaccination against, hepatitis infection, derived from strain HDB05, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen; HBsAg; hepatitis marker; virucide; hepatotropic;
antiinflammatory; DNA detection; vaccine; diagnostic;
hepatitis B virus infection; selectable marker; a-determinant.
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus genotype A HBsAg fragment.
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             Claim 3; SEQ ID NO 14; 61pp; German.
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130.00
95.65$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                  Sequence 60 AA;
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This sequence represents novel oligo- and poly-peptides that are variants of the hepatitis B surface antigen (HBBAG). HBV strain HBDO5 was isolated from a patient with inflammation of the liver but an atypical reaction pattern of hepatitis markers. PCR amplification and sequencing indicated the 5 specified mutations in the S gene, relative to adw wild-type. These mutations all caused amino acid variations: 4 in the a-determinant region of the other close to it at residue 181. The products of the invention have virucide, hepatotropic and antilnifiammatory activity. The products of the invention are used to detect specific antibodies, as probes or primers for detecting hepatitis B virus (HBV) nucleic acid, as immunogens and antibodies (Ab) raised against HBAG are used for detecting HBBAG including use in vaccination, diagnosis and screening of donated blood. The antibodies do not bind, or bind much less strongly, to the HBBAG from virus of genotype A, subtype adw. This sequence represents a fragment of HBPAG trus genotype A surface protein (HBBAG) a-determinant of corresponding to residues 101-170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
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Disclosure, Fig 1; 61pp; German.
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130.00
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91.30%
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Query Match:
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Disclosure; Fig 6; 61pp; German.

This sequence represents novel oligo- and poly-peptides that are variants of the hepatitis B surface antigen (HBBAQ). HBV strain HBDD5 was isolated from a patient with inflammation of the liver but an atypicial reaction pattern of hepatitis markers. PCR amplification and sequencing indicated the 5 specified mutations in the S gene, relative to adw wild-type. These mutations all caused amino acid variations: 4 in the a-determinant region and the other close to it at residue 181. The products of the invention have virucide, hepatotropic and antiinflammatory activity. The products of the invention are used to detect specific antibodies as probes or primers for detecting hepatitis B virus (HBV) nucleic acid, as immunogens and antibodies (Ab) raised against HBSAQ are used for detecting HBSAQ including use in vaccination, diagnosis and screening of donated blood. The antibodies do not bind, or bind much less strongly, to the HBSAQ from virus of genotype A, subtype adw. This sequence represents a fragment of the Hepatitus B virus wild-type HBD S surface protein (HBSAQ) S protein corresponding to residues 101-170. 

Sequence 70 AA;

12700 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.26e-10 130.00 95.65% 91.30% 93.53% Percent Similarity: Best Local Similarity: Query Match: Alignment Scores:

US-10-761-006A-1\_COPY\_527\_595 (1-69) x ADW68821 (1-70)

1 ACGACTCCTGCTCAAGGAAACTCTACGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC 60 25 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 44 셤 ò

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Search completed: December 27, 2005, 20:51:59 Job time : 20.262 secs

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Appli Appli Appli Appli Appl

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Sequence 5, Applarate No. 5196194
Sequence 1, Appli
                                                                                    Sequence 1, Appli
Sequence 3, Appli
Sequence 7, Appli
Patent No. 5196194
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Sequence 4, Appli
Sequence 12, Appli
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Patent No. 5164485
                                                                                                                                                                                                                                                        14, Appl
15, Appl
16, Appl
17, Appl
20, Appl
5198348
                                                                                                                                                                                    Sequence 7, A Sequence 6, A Sequence 9, A Sequence 13,
                                                                                                                                                                                                                                                       Sequence 14,
Sequence 15,
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND USES THEREOF
                                                                                                                                                             Sequence 5,
Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8,
Sequence 2,
                                                                      Sequence 3,
Sequence 1,
                                                                                                                                                                                                                                                                                                                               Sequence 20,
Patent No. 51
                                                                                                                                                                                                                                                                                                                Sequence
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                              5196194-18
US-08-760-797A-1
US-08-932-929B-1
US-08-932-929B-1
US-08-932-929B-1
US-09-193-104-5
US-09-193-104-6
US-09-193-104-14
US-09-193-104-14
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US-09-193-104-15
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US-09-193-104-12
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US-09-193-104-23
US-09-193-104-23
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US-09-193-104-23
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REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-193-104-8
US-08-447-591-2
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APPLICATION NUMBER: US/09/719,528A
FILING DATE: 30-Apr-2001
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/SG98/00046
FILING DATE: 19-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09719528A; Patent No. 6558675; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chong Jin
Gek Keow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen, Wei Ning
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                   US-09-719-528A-3
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Sequence 25, Appli
Sequence 25, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 21, Appli
Patent No. 5436139
Patent No. 5436139
                                                                                                                                         December 27, 2005, 20:44:58 ; Search time 4.6 Seconds (without alignments) 2480.270 Million cell updates/sec
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2: /cgn2 6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/H_COMB.pep:*
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6: /cgn2 6/ptodata/1/iaa/RE_COMB.pep:*
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                               using frame_plus_n2p model
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US-10_209-254-3

US-09-193-104-25

US-08-776-586-6

US-09-193-104-10

US-09-193-104-21

US-09-193-104-21

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US-09-721-480-3
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Maximum Match 100%
Listing first 45 summaries
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Kgapop 10.0 , Kgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length
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Alignment Scores:
Pred. No.:
                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 154
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US-08-776-585-6
                                                          Score:
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Patent No. 6787142

GENERAL TNFORMATION.

Lim, Gek Keow
Zhao, Yi
Chen, Wei Ning

TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: THE PC COMPATIONS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/209,264
FILING DATE: 31-Jul-2002
CLASSIFICATION NUMBER: PCT/SG98/00046
FILING DATA:
APPLICATION NUMBER: PCT/SG98/00046
FILING DATA:
APPLICATION NUMBER: DCT/SG98/00046
FILING DATA:
APPLICATION NUMBER: US/0066
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-013109-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   US-10-761-006A-1_COPY_527_595 (1-69) x US-09-719-528A-3 (1-400)
                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
TELEPHONE: (212) 708-1800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                        Gaps:
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ADDRESSER: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10023
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SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
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Best Local Similarity:
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Pred. No.:
                                                                                                                                            US-09-719-528A-3
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US-10-209-264-3
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Patent No. 5932426;
GENERAL INFORMATION:
APPLICANT: BARALLE, Francesco E.
APPLICANT: TSMINETZKY, Sergio
APPLICANT: TSMINETZKY, Sergio
TITLE OF INVENTION: MOLECULAR PRESENTING SYSTEM
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Larcher
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
 Length:
Matches:
Conservative:
Mismatches:
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133.00
95.65$
95.65$
1.91e-13
139.00
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Hepatitis B virus
US-09-193-104-25
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112 GlyAsnCys 114
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319 GlyAsnCys 321
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Best Local Similarity:
Query Match:
                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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// Sequence TO Application US/09193104A
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Sequence 20, Application US/09193104A
Sequence 20, Application US/09193104A
Sequence 20, Application US/09193104A
Sequence 20, Application US/09193104A
SAPLICANT: Primi, Daniele
APPLICANT: Priordalisi, Gianfranco
APPLICANT: Palla, Mario
TITLE OF INVENTION: Bacape Mutant of the Surface Antigen of Hepatitis ITILE OF INVENTION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-761-006A-1_COPY_527_595 (1-69) x US-09-193-104-10 (1-154)
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Matches:
Conservative:
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Mismatches:
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Indels:
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CURRENT APPLICATION NUMBER: US/09/193,104A
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: EP 97830635.5
BARLIER FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 44
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130.00
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112 GlyAenCys 114
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APPLICANT: Pizzo, Hanne
TITLE OF INVENTION IMMUNE RESPONSE MODULATOR ALPHA-2 MACROGLOBULIN COMPLEX
FILE REPERRACE: 2295-1-010CTP
CURRENT APPLICATION NUMBER: US/09/282,826A
CURRENT FILING DATE: 1999-03-31
BARLIER APPLICATION NUMBER: 09/053,301
BARLIER PILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 4
SOFTMARE: PATENTIN VET: 2.0
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                              STATE: D.C.
COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,585
FILING DATE: 31-MAR-1997
CLASSIFICATION: A35
PRICA APPLICATION NUMBER: WO PCT/EP95/03114
PILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REGISTRATION NUMBER: 69582/106
TELEPHONE: (202)672-5300
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; Sequence 3, Application US/09282826A
; Patent No. 6, 403092
; GENERAL INFORMATION:
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TELERA: (202)672-5399
TELEX: 904136
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 24 amino acids TYPE: amino acids STRANDEDNESS: single
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Best Local Similarity:
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; TYPE: PRT
; ORGANISM: HBSAG
US-09-282-826-3
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US-08-776-585-6
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Pred. No.:
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LENGTH: 226
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5436139-5
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| Sequence 21, Application US/09193104A |
| Patent No. 6172193 |
| Patent No. 6172193 |
| Patent No. 6172193 |
| APPLICANT: Prind, Daniele |
| APPLICANT: Prind, Mario |
| APPLICANT: Palla, Mario |
| TITLE OF INVENTION: Escape Mutant of the Surface Antigen of Hepatitis B |
| TITLE OF INVENTION: Virus |
| TITLE OF INVENTION: Virus |
| FILE REFERENCE: SBD1004US |
| CURRENT APPLICATION NUMBER: US/09/193,104A |
| CURRENT FILING DATE: 1998-11-16 |
| EARLIER FILING DATE: 1997-12-01 |
| NUMBER OF SEQ ID NOS: 44 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 21 |
| TYPE: PRT |
| TYPE: PRT |
| ORGANISM: Hepatitis B virus |
| ORGANISM: Hepatitis B virus |
| ORGANISM: Patentin Ver. 2.0 |
| ORGANISM: Hepatitis B virus |
| ORGANISM: Patentin Ver. 2.0 |
| ORGANISM: Patentin Ver. 2.0 |
| ORGANISM: Hepatitis B virus |
| ORGAN
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; Patent No. 5436139
; APPLICATI: RUTTER, WILLIAM J.; GOODMAN, HOWARD M. TITLE OF INVENTION: NON-PASSAGRABLE VIRUS
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
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                                                                            ; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-193-104-20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 154
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112 GlyAsnCys 114
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112 GlyAsnCys 114
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125 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 144
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Matches:
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Mismatches:
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APPLICATION NUMBER: US/058/89
PILING DATE: 08-JUL-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: 571,331
FILING DATE: 22-AUG-1990
APPLICATION NUMBER: 513,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 107,267
FILING DATE: 21-DEC-1979
APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979
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144 GlyAsnCys 146
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145 GlyAsnCys 147
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289 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 308
180 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysCysThrLysProThrAsp 199
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CTHER INFORMATION: Description of Artificial Sequence: pCMVII opti

CTHER INFORMATION: 330 E1/SAg

US-09-721-480-5
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TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,621
FILING DATE: -DEC-1984
PRIOR APPLICATION NUMBER: 13,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 10,267
FILING DATE: 21-JUL-1983
APPLICATION NUMBER: 10,267
FILING DATE: 24-JUL-1983
APPLICATION NUMBER: 11,099
APPLICATION NUMBER: 11,099
APPLICATION NUMBER: 21,099
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Matches:
Conservative:
Mismatches:
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APPLICANT: Glazer, Edward
APPLICANT: Houghton, Michael
TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
FILE REFERENCE: PP01635.002
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                                                                                                                     RESULT 13
US-09-7213-480-5
Sequence 5 Application US/09721480
; Patent No. 6740323
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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                                       61 GCAAACTGC 69
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Pred. No.:
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LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE: OTHER INFORMATION: Description of Artificial Sequence: plasmid OTHER INFORMATION: pCMVII-pS2-SA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-761-006A-1_COPY_527_595 (1-69) x US-09-721-480-3 (1-281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-761-006A-1_COPY_527_595 (1-69) x 5436139-5 (1-226)
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Matches:
Conservative:
Mismatches:
Indels:
    ; Patent No. 5436139

APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.:

TITLE OF INVENTION: NON-PASSAGEABLE VIRUS

NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACGACTCCTGCTCAAGGAACTCTACGTTTCCCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Selby, Mark
APPLICANT: Glazer, Edward
APPLICANT: Houghton, Michael
TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
FILE REFERENCE: PP01635.002
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/721,480
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/058/69,993
FILING DATE: 08-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 571,331
FILING DATE: 22-A06-1990
APPLICATION NUMBER: 513,055
FILING DATE: 12-JUL-1983
APPLICATION NUMBER: 107,267
FILING DATE: 21-DEC-1979
APPLICATION NUMBER: 41,909
FILING DATE: 24-MAY-1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mication US/09721480
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130.00
95.65%
91.30%
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93.53%
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145 GlyAsnCys 147
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Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                , LENGTH: 226
5436139-5
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Pred. No.:
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LENGTH: 281
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DB:
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Score:

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                                                                    32 ThrThrProAlaGlnGlyAsnSerMetPheProSerCysCysThrLysProThrAsp 341
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                                 US-10-761-006A-1_COPY_527_595 (1-69) x 5196194-18 (1-395)
                                                                                                                                                                                                                                Sequence 1. Application US/08760797A

Pateat No. 3928902
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: Ring of Prussia
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTENCY OF WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER: 08/42,612
APPLICATION NUMBER: 08/42,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAUMESTEE NITOR:
NAME: BAUMESTEE NUMBER: 33,833
REFERENCE/POCKET NUMBER: 33,833
REFERENCE/POCKET NUMBER: B45015-1C2
TELEDRONE: 610-270-5096
TELEBPAX: 610-270-5096
Gaps:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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130.00
95.65%
91.30%
                                                                                                                                    61 GGAAACTGC 69
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314 GlyAsnCys 316
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Best Local Similarity:
Query Match:
DB:
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US-08-760-797A-1
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Pred. No.:
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Db 342 GlyAsnCys 344
Search completed: December 27, 2005, 21:03:41
Job time: 4.6 secs
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